

FILE 'BIOSIS, MEDLINE' ORDERED AT 09:43:27 ON 15 JAN 200

L1 12 S (FGF19)  
L2 9 DUP REM L1 (3 DUPLICATES REMOVED)  
L3 62308 S FUSION (W) (POLYPEPTIDE? OR PROTEIN? OR POLYPROTEIN?)  
L4 167774 S L3 OR IMMUNOCONJUGATE? OR CONJUGATE?  
L5 244 S L4 (P) SAPORIN?  
L6 33 S L5 (P) (FGF)  
L7 0 S L6 AND (MYELOMA? OR OSTEOSARCOMA?)  
L8 15 S ((FGF2) OR (FGF3)) (W) RECEPTOR?  
L9 70327 S (MYELOMA? OR OSTEOSARCOMA?)  
L10 0 S L8 (P) L9  
L11 13 S L8 AND CELL?  
L12 8 DUP REM L11 (5 DUPLICATES REMOVED)  
L13 17 DUP REM L6 (16 DUPLICATES REMOVED)  
L14 4 S L13 AND PROLIFERATION?

09/424,080



<u>DB Name</u>	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u>
JPAB,EPAB,DWPI,TDBD	l29 and (myeloma\$ or osteosarcoma\$)	0	<u>L30</u>
JPAB,EPAB,DWPI,TDBD	l26 same (FGF)	15	<u>L29</u>
JPAB,EPAB,DWPI,TDBD	l25 same l26	0	<u>L28</u>
JPAB,EPAB,DWPI,TDBD	l25 and l26	0	<u>L27</u>
JPAB,EPAB,DWPI,TDBD	l24 same saporin\$	28	<u>L26</u>
JPAB,EPAB,DWPI,TDBD	((FGF) adj (18)) or (FGF18)	2	<u>L25</u>
JPAB,EPAB,DWPI,TDBD	l23 or immunoconjugate\$ or conjugate\$	58618	<u>L24</u>
JPAB,EPAB,DWPI,TDBD	fusion adj (polypeptide\$ or protein\$ or polyprotein\$)	4035	<u>L23</u>
JPAB,EPAB,DWPI,TDBD	cell\$ same (myeloma\$ or osteosarcoma\$) same ((FGF) adj receptor\$)	1	<u>L22</u>
USPT,PGPB	cell\$ same (myeloma\$ or osteosarcoma\$) same ((FGF) adj receptor\$)	2	<u>L21</u>
USPT,PGPB	cell\$ same (myeloma\$ or osteosarcoma\$) same ((FGF) same receptor\$)	5	<u>L20</u>
USPT,PGPB	cancer\$ same cell\$ same (myeloma\$ or osteosarcoma\$) same ((FGF) same receptor\$)	1	<u>L19</u>
USPT,PGPB	l14 and (proliferation\$ or proliferate\$)	16	<u>L18</u>
USPT,PGPB	l14 and (proliferation\$ or proliferate\$)	16	<u>L17</u>
USPT,PGPB	l14 and proliferation\$ or proliferate\$	8330	<u>L16</u>
USPT,PGPB	l14 and myeloma and osteosarcoma and cells	0	<u>L15</u>
USPT,PGPB	l13 same (FGF)	16	<u>L14</u>
USPT,PGPB	l6 same saporin\$	109	<u>L13</u>
USPT,PGPB	l11 and saporin\$	0	<u>L12</u>
USPT,PGPB	l6 and l9	2	<u>L11</u>
USPT,PGPB	l6 same l9	0	<u>L10</u>
USPT,PGPB	l7 or l8	3	<u>L9</u>
USPT,PGPB	(FGF18)	1	<u>L8</u>
USPT,PGPB	(FGF) adj (18)	3	<u>L7</u>
USPT,PGPB	l5 or immunoconjugate\$ or conjugate\$	75647	<u>L6</u>
USPT,PGPB	fusion adj (polypeptide\$ or protein\$ or polyprotein\$)	12704	<u>L5</u>
USPT	(FGF18)	1	<u>L4</u>
USPT	(FGF-18) same saporin\$	0	<u>L3</u>
USPT	l1 or immunoconjugate\$ or conjugate\$	73088	<u>L2</u>
USPT	fusion adj (polypeptide\$ or protein\$ or polyprotein\$)	12092	<u>L1</u>



<u>DB Name</u>	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u>
JPAB,EPAB,DWPI,TDBD	cyclosporin\$ same (FK506) same rapamycin same interferon\$	2	<u>L20</u>
USPT,PGPB	cyclosporin\$ same (FK506) same rapamycin same interferon\$	12	<u>L19</u>
USPT,PGPB	117 and (inflammat\$ or cancer\$ or autoimmune\$ or disease\$ or disorder\$)	88	<u>L18</u>
USPT,PGPB	116 and composition\$	88	<u>L17</u>
USPT,PGPB	cyclosporin\$ and (FK506) and rapamycin and interferon\$	100	<u>L16</u>
USPT,PGPB	114 and composition\$	11	<u>L15</u>
USPT,PGPB	113 and (cancer\$ or lymphoma\$ or leukemia\$ or myeloma\$ or denocarcinoma\$ or autoimmune\$ or (chronic inflammatory disease\$) or (rheumatoid arthritis) or (myasthenia gravis) or (lupus erythematosus) or uveitis or (hyperproliferative disease\$) or (psoriasis vulgaris))	14	<u>L14</u>
USPT,PGPB	112 same interferon\$.clm.	21	<u>L13</u>
USPT,PGPB	cyclosporin\$ or (FK506) or rapamycin.clm.	4096	<u>L12</u>
USPT,PGPB	110 and composition.clm.	20	<u>L11</u>
USPT,PGPB	18 same 19	27	<u>L10</u>
USPT,PGPB	interferon\$.clm.	1623	<u>L9</u>
USPT,PGPB	immunosuppressant\$ or cyclosporin\$ or (FK506) or rapamycin.clm.	5361	<u>L8</u>
USPT,PGPB	11 same interferon\$	349	<u>L7</u>
USPT,PGPB	15 and 14	12	<u>L6</u>
USPT,PGPB	11 and composition\$	4653	<u>L5</u>
USPT,PGPB	(bioactive adj peptide\$) and interferon\$	143	<u>L4</u>
USPT,PGPB	(bioactive adj peptide\$) or interferon\$	12223	<u>L3</u>
USPT,PGPB	(bioactive adj peptide\$) and interferon\$	143	<u>L2</u>
USPT,PGPB	immunosuppressant\$ or cyclosporin\$ or (FK506) or rapamycin	5450	<u>L1</u>

09/424,080



=> s cyclosporin? (p) (FK506) (p) rapamycin  
L3 736 CYCLOSPORIN? (P) (FK506) (P) RAPAMYCIN

=> s interferon? (w) (alpha or beta or omega or tao)  
L4 46367 INTERFERON? (W) (ALPHA OR BETA OR OMEGA OR TAO)

=> s l3 and l4  
L5 3 L3 AND L4

=> dup rem l5  
PROCESSING COMPLETED FOR L5  
L6 3 DUP REM L5 (0 DUPLICATES REMOVED)





GenCore version 4.5  
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OM protein - protein search, using SW model

Run on: January 15, 2002, 08:34:38 ; Search time 38.96 Seconds  
(without alignments)  
15.210 Million cell updates/sec

Title: US-09-424-080A-1

Perfect score: 42  
Sequence: 1 LTKKYPSP 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 50 summaries

Database :

A\_Geneseq\_1101.\*  
1: /SID58/gcgdata/geneseq/geneseq/AA1980.DAT:\*  
2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT:\*  
3: /SID58/gcgdata/geneseq/geneseq/AA1982.DAT:\*  
4: /SID58/gcgdata/geneseq/geneseq/AA1983.DAT:\*  
5: /SID58/gcgdata/geneseq/geneseq/AA1984.DAT:\*  
6: /SID58/gcgdata/geneseq/geneseq/AA1985.DAT:\*  
7: /SID58/gcgdata/geneseq/geneseq/AA1986.DAT:\*  
8: /SID58/gcgdata/geneseq/geneseq/AA1987.DAT:\*  
9: /SID58/gcgdata/geneseq/geneseq/AA1988.DAT:\*  
10: /SID58/gcgdata/geneseq/geneseq/AA1989.DAT:\*  
11: /SID58/gcgdata/geneseq/geneseq/AA1990.DAT:\*  
12: /SID58/gcgdata/geneseq/geneseq/AA1991.DAT:\*  
13: /SID58/gcgdata/geneseq/geneseq/AA1992.DAT:\*  
14: /SID58/gcgdata/geneseq/geneseq/AA1993.DAT:\*  
15: /SID58/gcgdata/geneseq/geneseq/AA1994.DAT:\*  
16: /SID58/gcgdata/geneseq/geneseq/AA1995.DAT:\*  
17: /SID58/gcgdata/geneseq/geneseq/AA1996.DAT:\*  
18: /SID58/gcgdata/geneseq/geneseq/AA1997.DAT:\*  
19: /SID58/gcgdata/geneseq/geneseq/AA1998.DAT:\*  
20: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT:\*  
21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT:\*  
22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	11	AA47561	Interferon-recepto
2	42	100.0	18	AA47562	Interferon-recepto
3	42	100.0	90	AA45587	Partial human inte
4	42	100.0	133	AA20109	Sequence encoded b
5	42	100.0	150	AA11799	Interferon alpha 8
6	42	100.0	162	AA30687	Sequence of hybrid
7	42	100.0	165	AA30687	Thrl4, Met16 mutan
8	42	100.0	165	AA43382	Human Interferon-a
9	42	100.0	165	AA43386	Human Interferon-a
10	42	100.0	165	AA43387	Human Interferon-a
11	42	100.0	165	AA43390	Human Interferon-a

12	42	100.0	165	AA43492	A human interferon
13	42	100.0	165	AA42887	N-terminal modifie
14	42	100.0	165	AA44828	Hybrid Interferon
15	42	100.0	165	AA44976	Human hybrid inter
16	42	100.0	166	AA30683	Synthetic human le
17	42	100.0	166	AA30684	Consensus human le
18	42	100.0	166	AA30685	Consensus human le
19	42	100.0	166	AA30686	Consensus human le
20	42	100.0	166	AA50229	Interferon alpha-1
21	42	100.0	166	AA50228	Sequence of Interf
22	42	100.0	166	AA60100	Sequence of hybrid
23	42	100.0	166	AA60102	Sequence of hybrid
24	42	100.0	166	AA60103	Sequence of hybrid
25	42	100.0	166	AA60304	Sequence of interf
26	42	100.0	166	AA60306	Hybrid alpha-inter
27	42	100.0	166	AA60186	Hybrid alpha-inter
28	42	100.0	166	AA60189	Hybrid alpha-inter
29	42	100.0	166	AA60189	Lymphoblastoid int
30	42	100.0	166	AA60189	Interferon-alpha-6
31	42	100.0	166	AA60189	Interferon-alpha-7
32	42	100.0	166	AA60189	Human interferon-a
33	42	100.0	166	AA60189	A human interferon
34	42	100.0	166	AA60189	Human interferon-a
35	42	100.0	166	AA60189	Human interferon-a
36	42	100.0	166	AA60189	Human interferon-a
37	42	100.0	166	AA60189	Human interferon-a
38	42	100.0	166	AA60189	Human interferon-a
39	42	100.0	166	AA60189	Human interferon-a
40	42	100.0	166	AA60189	Human interferon-a
41	42	100.0	166	AA60189	Human interferon-a
42	42	100.0	166	AA60189	Human interferon-a
43	42	100.0	166	AA60189	Human interferon-a
44	42	100.0	166	AA60189	Human interferon-a
45	42	100.0	166	AA60189	Human interferon-a
46	42	100.0	166	AA60189	Human interferon-a
47	42	100.0	166	AA60189	Human interferon-a
48	42	100.0	166	AA60189	Human interferon-a
49	42	100.0	166	AA60189	Human interferon-a
50	42	100.0	166	AA60189	Human interferon-a

#### ALIGNMENTS

RESULT 1  
ID AAR47561 standard; peptide: 11 AA.  
AC AAR47561;  
XX  
DT 12-JUL-1994 (first entry)  
DE Interferon-receptor binding peptide #4.  
XX  
XX IFN; cell surface receptor; pharmaceutical carrier molecule;  
KW drug delivery; neoplastic tissue; infection;  
KW Type I human interferon receptor complex.  
XX  
OS Synthetic.  
XX  
XX WO9401457-A.  
XX  
XX PD 20-JAN-1994.  
XX  
XX PF 06-JUL-1993; 93WO-CA00279.  
XX  
XX PR 07-JUL-1992; 92US-0905739.  
XX  
XX PR 20-NOV-1992; 92US-0980525.  
XX  
XX PA (FISH/) FISH E N.  
XX  
XX PI Fish EN;  
XX

DR WPI: 1994-034987/04.

XX New interferon receptor-binding peptide(s) - useful for  
PT delivering a pharmaceutically active drug to cells, e.g.  
PT neoplastic, infected or inflamed tissue cells

PS Claim 4; Page 35; 51pp; English.

XX The critical clusters of amino acids in the different IFN- $\alpha$ s and  
CC IFN- $\beta$  that interact with the Type 1 IFN receptor complex were  
CC defined. These critical peptide domains were used to design  
CC synthetic peptides AAR47558-R47564 that are useful as carriers for  
CC pharmaceutical compositions.

XX Sequence 11 AA;

Query Match Best Local Similarity 100.0%; Score 42; DB 15; Length 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSKSP 8

DB 2 ltekkysp 9

RESULT 2

AAR47562 ID AAR47562 standard; peptide; 18 AA.

XX AAR47562;

XX 12-JUL-1994 (first entry)

DE Interferon-receptor binding peptide #5.

KM IFN: cell surface receptor; pharmaceutical carrier molecule;

KM drug delivery; neoplastic tissue; infection;

XX Type 1 human Interferon receptor complex.

OS Synthetic.

XX WO9401457-A.

XX 20-JAN-1994.

XX 06-JUL-1993; 93WO-CA00279.

XX 07-JUL-1992; 92US-0909739.

XX 20-NOV-1992; 92US-0980525.

XX (FISH) FISH E N.

XX Fish EN;

XX WPI: 1994-034987/04.

XX New interferon receptor-binding peptide(s) - useful for  
PT delivering a pharmaceutically active drug to cells, e.g.  
PT neoplastic, infected or inflamed tissue cells

PS Claim 5; Page 35; 51pp; English.

XX The critical clusters of amino acids in the different IFN- $\alpha$ s and  
CC IFN- $\beta$  that interact with the Type 1 IFN receptor complex were  
CC defined. These critical peptide domains were used to design  
CC synthetic peptides AAR47558-R47564 that are useful as carriers for  
CC pharmaceutical compositions.

XX Sequence 18 AA;

Query Match

100.0%; Score 42; DB 15; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSKSP 8

DB 9 ltekkysp 16

RESULT 3

AAY55987 ID AAY55987 standard; Protein; 90 AA.

XX AAY55987;

XX 15-MAR-2000 (first entry)

DE Partial human interferon- $\alpha$ 5 protein.

KM Antiviral; anticancer; antiproliferative; human; interferon- $\alpha$ 5;

KM hepatic disease; hepatitis C; viral cirrhosis; hepatocellular carcinoma;

XX liver; gene expression.

OS Homo sapiens.

XX WO9598143-A1.

XX 18-NOV-1999.

XX 13-MAY-1999; 99WO-ES00134.

XX 13-MAY-1998; 98ES-0001003.

XX (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.

XX Prieto Valtuena J, Civeira Murillo MP, Larrea Leoz E;

XX WPI: 2000-038959/03.

XX N-PSDB: AAZ47031.

XX Treating liver diseases with interferon- $\alpha$ 5 or nucleic acid encoding

XX it, particularly chronic hepatitis C -

XX Disclosure; Page 30; 36pp; Spanish.

XX This sequence corresponds to a fragment of the human interferon- $\alpha$ 5  
CC protein (GenBank Accession No: X02956). The invention relates to a  
CC method of using interferon- $\alpha$ 5 or its coding sequence to prepare  
CC compositions for treatment of hepatic diseases, e.g. (i) chronic  
CC hepatitis C; (ii) cirrhosis of viral origin and (iii) hepatocellular  
CC carcinoma. The method restores the level of interferon- $\alpha$ 5, which  
CC is reduced in diseased liver cells, to normal levels.

XX Sequence 90 AA;

Query Match Best Local Similarity 100.0%; Score 42; DB 21; Length 90;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSKSP 8

DB 74 ltekkysp 81

RESULT 4

AAP20109 ID AAP20109 standard; Protein; 133 AA.

XX AAP20109;

XX 10-AUG-1992 (first entry)

DE Sequence encoded by leukocyte interferon LeIF G cDNA.



PT New hybrid alpha-interferon with enhanced antiviral activity -  
PT prepd. by recombinant DNA procedures  
XX  
PS Claim 2; Page 22; 26pp; English.  
XX  
CC The hybrid alpha-IFN of the invention includes different portions of  
CC two different naturally occurring alpha-IFN as joined discrete sub-  
CC sequences. They are defined and arranged as a delta-4 alpha-2  
CC (Bgl II-1) sub-segment preceding a (Bgl II) alpha-1 segment. It has  
CC an antiviral activity of at least 100,000,000 units/mg by cytopathic  
CC effect-inhibition assay. Dose is 100,000 - 1000,000 units/square  
CC metre body surface daily topically. The N-terminal Met is optional.  
CC The claimed DNA sequence coding for the hybrid alpha-IFN may differ  
CC in accordance with the degeneracy of the genetic code.  
XX  
SQ Sequence 162 AA;

Query Match 100.0%; Score 42; DB 6; Length 162;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LTERKXSP 8  
DB 127 ltekxsp 134

RESULT 7  
AAP30687  
ID AAP30687 standard; Protein; 165 AA.  
XX  
AC AAP30687;  
XX  
DT 10-SEP-1992 (first entry)  
XX  
DE Thr14, Met16 mutant human leukocyte interferon subtype F.  
XX  
KW Mutation; human; IFN.  
XX  
OS Synthetic.  
XX  
FH Key 14 Location/Qualifiers  
FT Region 16 /note= "mutation, Ala -> Thr"  
FT Region 16 /note= "mutation, Ile -> Met"  
XX  
XX MO8304053-A.  
XX  
PD 24-NOV-1983.  
XX  
PF 25-APR-1983; 83WO-US00605.  
XX  
PR 15-APR-1983; 83US-0483451.  
PR 06-MAY-1982; 82US-0375494.  
PR 12-DEC-1983; 83US-0560495.  
PR 21-SEP-1987; 87US-0099096.  
PR 01-JAN-1990; 90EP-0124236.  
XX  
PA (AMGE-) AMGEN INC.  
PA (AMGE-) AMGEN.  
PA (MOLE-) APPL MOLECULAR GENE.  
XX  
PI Alton NK, Peters MA, Stabinsky Y, Snilman DL;  
XX  
DR WPI; 1983-833208/48.  
XX  
XX Construction of large structural genes - useful in prepn. of  
XX human leukocyte interferon and analogues  
XX  
PS Claim 46; Page 85; 94pp; English.  
CC The sequence is that of a polypeptide which differs from human

CC Leukocyte interferon subtype F by two amino acid substitutions.  
CC It may be recombinantly produced in micro organisms transformed  
CC with the manufactured gene encoding it. See also AAP30673-P30686.  
XX  
SQ Sequence 165 AA;

Query Match 100.0%; Score 42; DB 4; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LTERKXSP 8  
DB 131 ltekxsp 138

RESULT 8  
AAW43382  
ID AAW43382 standard; protein; 165 AA.  
XX  
AC AAW43382;  
XX  
DT 07-APR-1998 (first entry)  
XX  
DE Human interferon-alpha 2b mutant (K132T).  
XX  
KW Gene delivery; interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;  
XX nucleic acid binding agent; targeted expression; mutant.  
XX  
OS Homo sapiens.  
XX  
PN WO9733998-A1.  
XX  
PD 18-SEP-1997.  
XX  
PF 14-MAR-1997; 97WO-US03846.  
XX  
PR 14-MAR-1996; 96US-0616023.  
XX  
PA (IMMU-) IMMUNE RESPONSE CORP.  
XX  
PI Carlo DJ, Chlou HC;  
XX  
DR WPI; 1997-470878/43.  
XX  
PT Delivering interferon gene to target mammalian cells in vivo or in  
PT vitro - as a molecular complex with a conjugate of nucleic acid  
PT binding agent and ligand for cell surface receptor, e.g. for  
PT treating virus infection or tumours  
XX  
PS Disclosure; Figure 11B; 52pp; English.  
XX  
XX This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)  
CC of mutant (K132T) which was recombinantly expressed in mice. A series  
CC of IFN-alpha 2b mutants were prepared with various single amino acid  
CC substitutions (AAW43382-90). The effect of these substitutions on  
CC antiviral activity (on mouse cells) for human IFN-alpha 2b was  
CC compared. This mutant had a relative activity of 0.1 compared with  
CC the native IFN-alpha 2b. The invention relates to a complex which  
CC targets expression of interferon in selected cells. The complex  
CC comprises the gene encoding interferon releasably linked to a conjugate  
CC of nucleic acid binding agent and a ligand which binds to a component on  
CC the surface of the cell. The method is used for targeted expression of  
CC recombinant IFN in selected cells, in vivo or in vitro, particularly for  
CC condyloma acuminatum, or for production of IFN for subsequent  
CC administration as exogenous protein.  
XX  
SQ Sequence 165 AA;

Query Match 100.0%; Score 42; DB 18; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTKKYS 8  
 |||||  
 DB 130 ltkkysp 137

## RESULT 9

AAW43386  
 ID AAW43386 standard; protein; 165 AA.

AC AAW43386;

DT 07-APR-1998 (first entry)

DE Human interferon-alpha 2b mutant (Q125R; K132T).

KW Gene delivery; interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;

KM nucleic acid binding agent; targeted expression; mutant.

XX Homo sapiens.

MO9733998-A1.

PD 18-SEP-1997.

PF 14-MAR-1997; 97WO-US03846.

PR 14-MAR-1996; 96US-0616023.

PA (IMMU-) IMMUNE RESPONSE CORP.

PI Carlo DJ, Chlou HC;

PS WPI; 1997-470878/43.

PT Delivering interferon gene to target mammalian cells in vivo or in

PT vitro - as a molecular complex with a conjugate of nucleic acid

PT binding agent and ligand for cell surface receptor, e.g. for

PT treating virus infection or tumours

PS Disclosure; Figure 11B; 52pp; English.

CC This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)

CC mutant (Q125R; K132T) which was recombinantly expressed in mice. A

CC series of IFN-alpha 2b mutants were prepared with various amino acid

CC substitutions (AAW43382-90). The effect of these substitutions on

CC antiviral activity (on mouse cells) for human IFN-alpha 2b was

CC compared. This mutant had a relative activity of 23 compared with

CC the native IFN-alpha 2b. The invention relates to a complex which

CC targets expression of interferon in selected cells. The complex

CC comprises the gene encoding interferon releasably linked to a conjugate

CC of nucleic acid binding agent and a ligand which binds to a component on

CC the surface of the cell. The method is used for targeted expression of

CC recombinant IFN in selected cells, in vivo or in vitro, particularly for

CC treatment of hepatitis, several forms of cancer and leukaemia and

CC condyloma acuminatum, or for production of IFN for subsequent

CC administration as exogenous protein.

SQ Sequence 165 AA;

Query Match 100.0%; Score 42; DB 18; Length 165;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTKKYS 8  
 |||||  
 DB 130 ltkkysp 137

RESULT 10

AAW43387

ID AAW43387 standard; protein; 165 AA.

AC AAW43387;

DT 07-APR-1998 (first entry)

DE Human interferon-alpha 2b mutant (R121K; Q125R; K132T).

KW Gene delivery; interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;

KM nucleic acid binding agent; targeted expression; mutant.

XX Homo sapiens.

MO9733998-A1.

PD 18-SEP-1997.

PF 14-MAR-1997; 97WO-US03846.

PR 14-MAR-1996; 96US-0616023.

PA (IMMU-) IMMUNE RESPONSE CORP.

PI Carlo DJ, Chlou HC;

PS WPI; 1997-470878/43.

PT Delivering interferon gene to target mammalian cells in vivo or in

PT vitro - as a molecular complex with a conjugate of nucleic acid

PT binding agent and ligand for cell surface receptor, e.g. for

PT treating virus infection or tumours

PS Disclosure; Figure 11B; 52pp; English.

CC This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)

CC mutant (R121K; K132T) which was recombinantly expressed in mice.

CC A series of IFN-alpha 2b mutants were prepared with various amino acid

CC substitutions (AAW43382-90). The effect of these substitutions on

CC antiviral activity (on mouse cells) for human IFN-alpha 2b was

CC compared. This mutant had a relative activity of 170 compared with

CC the native IFN-alpha 2b. The invention relates to a complex which

CC targets expression of interferon in selected cells. The complex

CC comprises the gene encoding interferon releasably linked to a conjugate

CC of nucleic acid binding agent and a ligand which binds to a component on

CC the surface of the cell. The method is used for targeted expression of

CC recombinant IFN in selected cells, in vivo or in vitro, particularly for

CC treatment of hepatitis, several forms of cancer and leukaemia and

CC condyloma acuminatum, or for production of IFN for subsequent

CC administration as exogenous protein.

SQ Sequence 165 AA;

Query Match 100.0%; Score 42; DB 18; Length 165;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTKKYS 8  
 |||||  
 DB 130 ltkkysp 137

RESULT 11

AAW43390

ID AAW43390 standard; protein; 165 AA.

AC AAW43390;

DT 07-APR-1998 (first entry)

DE Human interferon-alpha 2b mutant (Q125K; K132T).

KW Gene delivery; interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;

KW nucleic acid binding agent; targeted expression; mutant.  
 XX Homo sapiens.  
 OS  
 XX WO9733998-A1.  
 PN  
 XX 18-SEP-1997.  
 PD  
 XX 14-MAR-1997; 97WO-US03846.  
 PF  
 XX 14-MAR-1996; 96US-0616023.  
 PR  
 XX (IMMUNO-) IMMUNE RESPONSE CORP.  
 PA  
 XX Carlo DJ, Chlou HC;  
 PI  
 XX WPI; 1997-470878/43.  
 DR  
 XX  
 PT Delivering interferon gene to target mammalian cells in vivo or in  
 PT vitro - as a molecular complex with a conjugate of nucleic acid  
 PT binding agent and ligand for cell surface receptor, e.g. for  
 PT treating virus infection or tumours  
 PS Disclosure; Figure 11B; 52pp; English.  
 XX  
 XX This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)  
 CC mutant (Q125K; K132T) which was recombinantly expressed in mice. A  
 CC series of IFN-alpha 2b mutants were prepared with various amino acid  
 CC substitutions (AAW43382-90). The effect of these substitutions on  
 CC antiviral activity (on mouse cells) for human IFN-alpha 2b was  
 CC compared. This mutant had a relative activity of 45 compared with  
 CC the native IFN-alpha 2b. The invention relates to a complex which  
 CC targets expression of interferon in selected cells. The complex  
 CC comprises the gene encoding interferon releasably linked to a conjugate  
 CC of nucleic acid binding agent and a ligand which binds to a component on  
 CC the surface of the cell. The method is used for targeted expression of  
 CC recombinant IFN in selected cells, in vivo or in vitro, particularly for  
 CC treatment of hepatitis, several forms of cancer and leukemia and  
 CC condyloma acuminatum, or for production of IFN for subsequent  
 CC administration as exogenous protein.  
 CC  
 XX Sequence 165 AA;  
 SQ

Query Match 100.0%; Score 42; DB 18; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKRYSP 8  
 |||||  
 DB 130 ltekkySP 137

RESULT 12  
 AAY43492  
 ID AAY43492 standard; Protein; 165 AA.  
 AC  
 XX AAY43492;  
 AC  
 XX 26-JAN-2000 (first entry)  
 DT  
 XX A human interferon-alpha (IFN-alpha) protein.  
 DE  
 XX Interferon-alpha-2b; IFN-alpha; avb3 antagonist; avb3 receptor ligand;  
 KW metastasis-associated receptor ligand; angiogenesis; cell proliferation;  
 KW anti-angiogenic protein; avb3-integrin; cancer; arthritis;  
 KW macular degeneration; diabetic retinopathy; hemangioma; psoriasis;  
 KW osteoporosis; thrombosis; angina; atherosclerosis; antiviral;  
 KW antibacterial; antifungal.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO9951638-A1.  
 PN

XX  
 PD 14-OCT-1999.  
 XX  
 XX 07-APR-1999; 99WO-US04295.  
 PF  
 XX 08-APR-1998; 98US-0081074.  
 PR  
 XX (SEAR ) SEARLE & CO G D.  
 PA  
 XX Tjoeng FS, Fok KF;  
 PI  
 XX WPI; 1999-620196/53.  
 DR  
 XX  
 PT New conjugates of integrin antagonist and ligand for  
 PT metastasis-associated receptor, for treating angiogenesis-related  
 PT diseases, e.g. cancer  
 PS Claim 12; Page 102; 108pp; English.  
 XX  
 XX The present sequence represents an interferon-alpha (IFN-alpha) protein,  
 CC and can be conjugated to the avb3 antagonists of the invention. The  
 CC specification describes pharmaceutical compounds and their salts which  
 CC are dual avb3 receptor/metastasis-associated receptor ligands. These  
 CC compounds inhibit angiogenesis and thus proliferation of (cancer) cells.  
 CC One component binds to the avb3 receptor and the other to a  
 CC metastasis-associated receptor. The avb3 antagonists may also be  
 CC conjugated to anti-angiogenic proteins, such as IFN-alpha and its  
 CC derivatives. The compounds are used to treat angiogenesis-related  
 CC disorders (mediated by the avb3-integrin), specifically cancer (of lung,  
 CC breast, ovary, prostate, stomach, colon, kidney or bladder, also  
 CC melanoma, hepatoma, sarcoma and lymphoma), arthritis and macular  
 CC degeneration, and also diabetic retinopathy, hemangioma, psoriasis,  
 CC osteoporosis, thrombosis, angina, atherosclerosis etc. The compounds may  
 CC also be useful as antiviral, antibacterial and antifungal agents.  
 CC  
 XX Sequence 165 AA;  
 SQ

Query Match 100.0%; Score 42; DB 20; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKRYSP 8  
 |||||  
 DB 130 ltekkySP 137

RESULT 13  
 AAY82887  
 ID AAY82887 standard; Protein; 165 AA.  
 AC  
 XX AAY82887;  
 AC  
 XX 25-JUL-2000 (first entry)  
 DT  
 XX N-terminal modified interferon alpha A/D hybrid.  
 DE  
 XX Biconjugate: a.vb\_3 integrin; interferon alpha; angiogenesis;  
 KW cancer; tumour; osteoporosis; Paget's disease; Kaposi's sarcoma;  
 KW periodontal disease; metastasis; neoplasia; retinopathy; arthritis;  
 KW psoriasis; leukemia; malignant melanoma; atherosclerosis;  
 KW smooth muscle cell migration; inhibition; treatment; antagonist;  
 KW angina; thrombosis; restenosis; antiviral; antifungal;  
 KW antibacterial.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200009143-A1.  
 PN  
 XX 24-FEB-2000.  
 PD  
 XX 07-APR-1999; 99WO-US04296.  
 PF  
 XX

PR 13-AUG-1998; 98US-0096442.  
 XX  
 XX (SEAR ) SEARLE & CO G D.  
 XX  
 XX Fok KF, Tjoeng FS;  
 PI  
 XX WPI: 2000-205894/18.  
 DR N-PSDB; AA293036.  
 XX  
 XX New bioconjugates comprising an avb3 antagonist and a  
 PT metastatic-associated receptor ligand, useful for treating cancer and  
 PT other angiogenic diseases, or as antiviral, antifungal or antibacterial  
 PT agents  
 XX  
 XX Claim 13; Page 111; 123pp; English.  
 PS  
 CC Bioconjugates comprising one or more a.vb.3 antagonist moieties  
 CC coupled to a peptide or polypeptide having anti-angiogenic properties  
 CC can be used for treating a human patient with an  
 CC angiogenesis-mediated disease, e.g. cancer, arthritis, or macular  
 CC degeneration. The a.vb.3 integrin is normally associated with  
 CC endothelial cells but can promote the formation of blood vessels  
 CC (angiogenesis) in tumours. The a.vb.3 integrin is also known to  
 CC play a role in tumour metastasis, neoplasia, osteoporosis,  
 CC Paget's disease, retinopathy, arthritis, periodontal disease,  
 CC psoriasis and smooth muscle cell migration. Interferon alpha is a  
 CC family of proteins which possess complex antiviral, antineoplastic  
 CC and immunomodulating activities. Interferon alpha is effective  
 CC against a variety of cancers including hairy cell leukaemia,  
 CC chronic myelogenous leukaemia, malignant melanoma and Kaposi's  
 CC sarcoma. Multi-functional bioconjugates comprising both a.vb.3  
 CC antagonists and interferon alpha 2b can exhibit greater biological  
 CC activity when compared to a single factor or having improved  
 CC half-life or decreased adverse side effects, or a combination of  
 CC these properties. They can be used for inhibiting elevated levels  
 CC of tumor antigens, inhibiting the proliferation of tumor cells and  
 CC inhibiting tumor growth. The bioconjugates can also be used for  
 CC treating e.g. osteoporosis, humoral hypercalcemia of malignancy,  
 CC Paget's disease, retinopathy including diabetic retinopathy,  
 CC arthritis, including rheumatoid arthritis, periodontal disease,  
 CC psoriasis, thrombosis, angina, atherosclerosis, smooth muscle cell  
 CC migration and restenosis in a mammal. They are also useful as  
 CC antiviral, antifungal and antibacterial agents. PMON20433 is a  
 CC modified version of PMON20405 (See AA293035) such that the amino  
 CC terminus of interferon alpha A/D is Met-Cys-IFN alpha A/D as  
 CC opposed to Met-Ala-Cys-IFN alpha A/D.  
 CC  
 CC Sequence 165 AA:  
 SQ  
 Query Match 100.0%; Score 42; DB 21; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LTERKXSP 8  
 DB 130 lterkxsp 137  
 RESULT 14  
 AA444828  
 ID AA444828 standard; Protein; 165 AA.  
 XX  
 AC AA444828;  
 XX  
 XX 18-MAY-2000 (first entry)  
 DT  
 XX  
 DE Hybrid interferon fusion protein HY-3.  
 XX  
 XX Hybrid interferon-alpha protein; HY-3; IFN-alpha; antiviral;  
 KW antiproliferative; influenza; hepatitis B; cell growth regulation;  
 KW tumour; cancer; osteogenic sarcoma; multiple myeloma.  
 XX

OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN W0200006735-A1.  
 XX  
 PD 10-FEB-2000.  
 XX  
 PF 06-JUL-1999; 99WO-US15284.  
 XX  
 PR 28-JUL-1998; 98US-0094407.  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Zoon KC, Hu R, Bekisz JB, Hayes MP;  
 PI  
 XX WPI: 2000-183128/16.  
 DR N-PSDB; AA250311.  
 XX  
 PT New hybrid interferon-alpha polypeptides with interferon-alpha  
 PT biological activity, useful to treat viral diseases  
 PS  
 PS Claim 8; Fig 5; 72pp; English.  
 XX  
 CC The present sequence is hybrid interferon fusion protein HY-3,  
 CC comprising IFN-alpha 2c (amino acid residues 96-166) and IFN-alpha21a  
 CC (amino acid residues 1-95). This is used as an antiviral and  
 CC antiproliferative agent. Hybrid IFN-alpha (interferon-alpha) proteins  
 CC are used in the treatment of viral diseases e.g. influenza, hepatitis B,  
 CC or to regulate cell growth, especially tumour cell growth e.g. in tumour  
 CC treatment and cancers like osteogenic sarcoma, multiple myeloma etc.  
 CC They are transformed into host cells using vectors. Pharmaceutically  
 CC acceptable carriers can be included with hybrid IFN-alpha for  
 CC therapeutic administration.  
 CC  
 CC Sequence 165 AA:  
 SQ  
 Query Match 100.0%; Score 42; DB 21; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LTERKXSP 8  
 DB 130 lterkxsp 137  
 RESULT 15  
 AA444976  
 ID AA444976 standard; Protein; 165 AA.  
 XX  
 AC AA444976;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE Human hybrid interferon alpha, HY-3.  
 XX  
 XX Human; Interferon alpha; HuIFNalpha; hybrid; HY-3; IFN-alpha21a; tumour;  
 KW IFN-alpha2c; cytostatic; antiviral; antiproliferative; immunomodulator;  
 KW treatment; viral disease; encephalomyocarditis; influenza; rabies;  
 KW respiratory tract infection; viral zoonoses; arbovirus infection;  
 KW Herpes simplex; Varicella zoster; keratitis; Hodgkin's disease; cancer;  
 KW acute haemorrhagic conjunctivitis; hepatitis B; hepatitis C; lymphoma;  
 KW osteogenic sarcoma; multiple myeloma; leukaemia; carcinoma; melanoma;  
 KW papilloma.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 1..95  
 FT Region /note="Derived from IFN-alpha2c"  
 FT Domain /note="Domain affecting antiproliferative activity"  
 FT





XX 24-NOV-1983.  
PD  
XX  
PF 25-APR-1983; 83WO-US00605.  
XX  
PR 15-APR-1983; 83US-0483451.  
PR 06-MAY-1982; 82US-0375494.  
PR 12-DEC-1983; 83US-0560495.  
PR 21-SEP-1987; 87US-009096.  
PR 01-JAN-1990; 90EP-0124236.  
XX  
PA (AMGE-) AMGEN INC.  
PA (AMGE-) AMGEN.  
PA (MOLE-) APPL MOLECULAR GENE.  
XX  
PI Alton NK, Peters MA, Stabinsky Y, Sultman DL;  
XX  
DR WPI: 1983-833208/48.  
PF Construction of large structural genes - useful in prepn. of  
human leukocyte interferon and analogues

Claim 38; Page 84; 94pp; English.

XX  
CC The sequence is that of a consensus human leukocyte interferon,  
CC encoded by a gene manufactured such that it is capable of directing  
CC synthesis of the interferon in a selected host microorganism.  
CC See also AAP30673-P30687.  
XX  
SQ Sequence 166 AA;

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LLEKKYSP 8  
DB 131 ltekkyssp 138  
SQ

RESULT 18  
AAP30685  
ID AAP30685 standard; Protein; 166 AA.  
XX  
AC AAP30685;  
XX  
DT 10-SEP-1992 (first entry)

Consensus human leukocyte interferon #2.

KW Mutation; human; IFN.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT 14  
FT Region /note= "mutation, Ala -> Thr"  
FT 16  
FT Region /note= "mutation, Ile -> Met"  
FT 22  
FT Region /note= "mutation, Gly -> Arg"  
FT 76  
FT Region /note= "mutation, Thr -> Ala"  
FT 78  
FT Region /note= "mutation, Glu -> Asp"  
FT 79  
FT Region /note= "mutation, Gln -> Glu"  
FT 86  
FT Region /note= "mutation, Ser -> Tyr"  
FT 90  
FT Region /note= "mutation, Asn -> Tyr"  
FT 96  
FT Region

FT /note= "mutation, Met -> Leu"  
FT 156  
FT Region /note= "mutation, Lys -> Thr"  
FT 157  
FT Region /note= "mutation, Ile -> Asn"  
FT 158  
FT Region /note= "mutation, Phe -> Leu"  
XX  
PN W08304053-A.  
XX  
PD 24-NOV-1983.  
XX  
PF 25-APR-1983; 83WO-US00605.  
XX  
PR 15-APR-1983; 83US-0483451.  
PR 06-MAY-1982; 82US-0375494.  
PR 12-DEC-1983; 83US-0560495.  
PR 21-SEP-1987; 87US-009096.  
PR 01-JAN-1990; 90EP-0124236.  
XX  
PA (AMGE-) AMGEN INC.  
PA (AMGE-) AMGEN.  
PA (MOLE-) APPL MOLECULAR GENE.

XX  
PI Alton NK, Peters MA, Stabinsky Y, Sultman DL;  
XX  
DR WPI: 1983-833208/48.  
XX  
PF Construction of large structural genes - useful in prepn. of  
human leukocyte interferon and analogues

Claim 38; Page 84; 94pp; English.

XX  
CC The sequence is that of a consensus human leukocyte interferon,  
CC encoded by a gene manufactured such that it is capable of directing  
CC synthesis of the interferon in a selected host microorganism.  
CC See also AAP30673-P30687.  
XX  
SQ Sequence 166 AA;

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LLEKKYSP 8  
DB 131 ltekkyssp 138  
SQ

RESULT 19  
AAP30686  
ID AAP30686 standard; Protein; 166 AA.  
XX  
AC AAP30686;  
XX  
DT 10-SEP-1992 (first entry)

Consensus human leukocyte interferon #3.

KW Mutation; human; IFN.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT 22  
FT Region /note= "mutation, Gly -> Arg"  
FT 76  
FT Region /note= "mutation, Thr -> Ala"  
FT 78  
FT Region /note= "mutation, Glu -> Asp"  
FT 79  
FT Region /note= "mutation, Gln -> Glu"

FT	Region	86	/note= "mutation, Ser -> Tyr"
FT	Region	90	/note= "mutation, Asn -> Tyr"
FT	Region	96	/note= "mutation, Met -> Leu"
FT	Region	114	/note= "mutation, Asn -> Tyr"
FT	Region	121	/note= "mutation, Met -> Leu"
FT	Region	156	/note= "mutation, Lys -> Thr"
FT	Region	157	/note= "mutation, Ile -> Asn"
FT	Region	158	/note= "mutation, Phe -> Leu"
XX			
PN	W08304053-A.		
XX			
XX	24-NOV-1983.		
XX			
PF	25-APR-1983;	83WO-US00605.	
XX			
PR	15-APR-1983;	83US-0483451.	
PR	06-MAY-1982;	82US-0375494.	
PR	12-DEC-1983;	83US-0560495.	
PR	21-SEP-1987;	87US-0099096.	
PR	01-JAN-1990;	90EP-0124236.	
XX			
PA	(AMGE-) AMGEN INC.		
PA	(AMGE-) AMGEN.		
PA	(MOLE-) APPL MOLECULAR GENE.		
XX			
PI	Alton NK, Peters MA, Stabinsky Y, Snilman DL;		
XX			
DR	WPI; 1983-833208/48.		
XX			
PT	Construction of large structural genes - useful in prepn. of		
PT	human leukocyte interferon and analogues		
XX			
PS	Claim 38; Page 84; 94pp; English.		
XX			
CC	The sequence is that of a consensus human leukocyte interferon,		
CC	encoded by a gene manufactured such that it it capable of directing		
CC	synthesis of the interferon in a selected host microorganism.		
CC	See also AAP30673-P30687.		
XX			
Q	Sequence 166 AA;		
Q			
Query Match	100.0%;	Score 42;	DB 4; Length 166;
Best Local Similarity	100.0%;	Pred. NO. 1.3;	
Matches 8; Conservative	0;	Mismatches	0; Indels 0; Gaps 0.
OY	1 LTERKSP 8		
DB	131 lterkysp 138		
RESULT 20			
AAP50229			
ID	AAP50229 standard; Protein; 166 AA.		
XX			
AC	AAP50229;		
XX			
DT	24-NOV-1991 (first entry)		
XX			
DE	Interferon alpha-1.		
XX			
KW	' Interferon alpha-1; hybrid protein; crossover region.		
XX			
Key	Location/Qualifiers		
FT	Region	63..66	

FT	Region	/label= crossover region A 88..95
FT	Region	/label= crossover region B 88..101
FT	Region	/label= crossover region C 88..106
FT	Region	/label= crossover region D 109..113
FT	Region	/label= crossover region E 114..117
FT	Region	/label= crossover region F 126..131
FT	Region	/label= crossover region G 133..151
FT	Region	/label= crossover region H 153..154
FT	Region	/label= crossover region I 155..161
FT	Region	/label= crossover region J
XX		Epi41484-A.
XX		15-MAY-1985.
XX		05-JUN-1984; 84EP-0303787.
XX		10-JUN-1983; 83GB-0015980.
PA	(BIOJ ) BIOGEN NV.	
XX	Weissmann C, Weber H;	
XX	WPI; 1985-117654/20.	
DR	N-PSDB; AAN50273.	
XX	New hybrid DNA sequences and hybrid polypeptide(s) - useful in prodn. of interferon(s), lymphokines, viral antigens, etc.	
XX		
PS	Disclosure; Fig. 6A-C; 47pp; English.	
CC	The DNA encoding interferon alpha-1 may be fused to a second coding sequence, eg for animal or human alpha, beta or gamma- interferons, lymphokines, foot-and-mouth disease antigens, to form a hybrid DNA. The DNA must be fused to the second DNA sequence in the same reading frame to maintain a constant reading frame through a crossover region common to both sequences. The hybrid sequences are obd. without the need for chance availability of restriction sites to be combined. Segmental deletions to give prods. with modified properties, activity and specificity are reliable.	
SO	Sequence 166 AA:	
OY	Query Match 100.0%; Score 42; DB 6; Length 166; Best Local Similarity 100.0%; Pred. No. 1.3; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	1 LTERKYP 8 131 lterkyp 138	
RESULT 21		
AAP60828	ID AAP60828 standard; Protein: 166 AA.	
XX	AAP60828;	
XX	AC AC	
DT	26-JUL-1991 (first entry)	
DE	Sequence of interferon-alpha 1.	
XX	Hepatitis B therapy; Kerato-conjunctivitis epidemica;	

KM Viral disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN DE3603958-A.  
 XX  
 PD 14-AUG-1986.  
 XX  
 PF 07-FEB-1986; 86DE-3603958.  
 XX  
 PR 08-FEB-1985; 85JP-0024050.  
 XX  
 PA (GRRC ) GREEN CROSS CORP.  
 XX  
 PI Yamauchi TY, Masaki AH, Nagai MY, Arimura HT, Suyama T;  
 DR WPI; 1986-219704/34.  
 DR N-PSDB; AAN60747.  
 XX  
 PT DNA sequence of interferon alpha one - and recombinant plasmid and  
 transformation, giving peptide for use in treating viral diseases  
 e.g. hepatitis and kerato conjunctivitis epidemica  
 PS Disclosure; Page 2-3; 42pp; German.  
 XX  
 CC Known interferon-alpha one has aspartic acid as AA 35 and the DNA  
 CC which codes for this AA is GAC. The interferon-1 one of the  
 CC invention has asparagine as AA 35 and the DNA which codes for this  
 CC AA is AAC.  
 XX  
 SQ Sequence 166 AA;

Query Match 100.0%; Score 42; DB 7; Length 166;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LTERKXSP 8  
 |||||||  
 Db 131 lterkxsp 138

RESULT 22  
 ID AAP60100 standard; Protein; 166 AA.  
 XX  
 AC AAP60100;  
 XX  
 PF 07-AUG-1991 (first entry)  
 DE Sequence of hybrid human lymphoblastoid interferons (LYIFN) alpha-2  
 and alpha-3, B1B2D3B4.  
 XX  
 KW Antiviral agent; neoplastic agent; therapy.  
 OS Homo sapiens.  
 XX  
 PN EP205404-A.  
 XX  
 PD 17-DEC-1986.  
 XX  
 PF 05-JUN-1986; 86EP-0810243.  
 XX  
 PR 11-JUN-1985; 85GB-0014726.  
 XX  
 PA (CIBA ) CIBA GEIGY AG.  
 XX  
 PI Meyer F, Hinnen A, Meister A, Grutter MK, Alkan S;  
 DR WPI; 1986-333879/51.  
 DR  
 PT New hybrid lymphoblastoid interferon(s) - useful as antiviral and  
 neoplastic agents.

XX  
 PS Claim 3; Page 72; 82pp; English.  
 XX  
 CC The hybrid polypeptides of the invention have an AA sequence composed  
 CC of 2-4 sub-sequences corresp. in AA identity and number to sub-  
 CC sequences of LYIFN-alpha-2 and LYIFN-alpha-3. In particular, the  
 CC claimed polypeptides have the AA sequence of : (i) AAs 1-150 of  
 CC -alpha-2 and 151-166 of -alpha-3; (ii) AAs 1-92 of -alpha-2, 93-150  
 CC of -alpha-3 and 151-166 of -alpha-2 or (iii) AAs 1-60 of -alpha-2,  
 CC 61-92 of -alpha-3, 93-150 of -alpha-2 or -alpha-3 and 151-166 of  
 CC -alpha-2 or -alpha-3. AAP60099-P60104 are specifically claimed.  
 XX  
 SQ Sequence 166 AA;

Query Match 100.0%; Score 42; DB 7; Length 166;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LTERKXSP 8  
 |||||||  
 Db 131 lterkxsp 138

RESULT 23  
 ID AAP60102 standard; Protein; 166 AA.  
 XX  
 AC AAP60102;  
 XX  
 DT 07-AUG-1991 (first entry)  
 DE Sequence of hybrid human lymphoblastoid interferons (LYIFN) alpha-2  
 and alpha-3, B1B2D3B4.  
 XX  
 KW Antiviral agent; neoplastic agent; therapy.  
 OS Homo sapiens.  
 XX  
 PN EP205404-A.  
 XX  
 PD 17-DEC-1986.  
 XX  
 PF 05-JUN-1986; 86EP-0810243.  
 XX  
 PR 11-JUN-1985; 85GB-0014726.  
 XX  
 PA (CIBA ) CIBA GEIGY AG.  
 XX  
 PI Meyer F, Hinnen A, Meister A, Grutter MK, Alkan S;  
 DR WPI; 1986-333879/51.  
 DR  
 PT New hybrid lymphoblastoid interferon(s) - useful as antiviral and  
 neoplastic agents.  
 XX  
 PS Claim 5; Page 73; 82pp; English.  
 XX  
 CC The hybrid polypeptides of the invention have an AA sequence composed  
 CC of 2-4 sub-sequences corresp. in AA identity and number to sub-  
 CC sequences of LYIFN-alpha-2 and LYIFN-alpha-3. In particular, the  
 CC claimed polypeptides have the AA sequence of : (i) AAs 1-150 of  
 CC -alpha-2 and 151-166 of -alpha-3; (ii) AAs 1-92 of -alpha-2, 93-150  
 CC of -alpha-3 and 151-166 of -alpha-2 or (iii) AAs 1-60 of -alpha-2,  
 CC 61-92 of -alpha-3, 93-150 of -alpha-2 or -alpha-3 and 151-166 of  
 CC -alpha-2 or -alpha-3. AAP60099-P60104 are specifically claimed.  
 XX  
 SQ Sequence 166 AA;

Query Match 100.0%; Score 42; DB 7; Length 166;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTKKXSP 8  
 |||||  
 DB 131 ltkkxsp 138

## RESULT 24

AAP60103  
 ID AAP60103 standard; Protein; 166 AA.

XX  
 AC AAP60103;

DT 07-AUG-1991 (first entry)

DE Sequence of hybrid human lymphoblastoid interferons (LYIFN) alpha-2  
 and alpha-3, BID2D3D4.

XX Antiviral agent; neoplastic agent; therapy.

XX Homo sapiens.

PN EP205404-A.

PD 17-DEC-1986.

PF 05-JUN-1986; 86EP-0810243.

PR 11-JUN-1985; 85GB-0014726.

PA (CIBA ) CIBA GEIGY AG.

PI Meyer F, Hinnen A, Meister A, Grutter MK, Alkan S;

DR WPI; 1986-333879/51.

PT New hybrid lymphoblastoid interferon(s) - useful as antiviral and  
 neoplastic agents.

PS Claim 6; Page 73; 82pp; English.

XX The hybrid polypeptides of the invention have an AA sequence composed  
 CC of 2-4 sub-sequences corresp. in AA identity and number to sub-  
 CC sequences of LYIFN-alpha-2 and LYIFN-alpha-3. In particular, the  
 CC claimed polypeptides have the AA sequence of : (i) AAs 1-150 of  
 CC -alpha-2 and 151-166 of -alpha-3; (ii) AAs 1-92 of -alpha-2, 93-150  
 CC of -alpha-3 and 151-166 of -alpha-2 or (iii) AAs 1-60 of -alpha-2,  
 CC 61-92 of -alpha-3, 93-150 of -alpha-2 or -alpha-3 and 151-166 of  
 CC -alpha-2 or -alpha-3. AAP60099-P60104 are specifically claimed.

SQ Sequence 166 AA;

Query Match 100.0%; Score 42; DB 7; Length 166;

Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTKKXSP 8  
 |||||  
 DB 131 ltkkxsp 138

## RESULT 25

AAP60304  
 ID AAP60304 standard; Protein; 166 AA.

XX  
 AC AAP60304;

DT 23-AUG-1991 (first entry)

DE Sequence of interferon (IFN) alpha S51B10.

XX Antiviral; antitumour.

XX

OS Homo sapiens.

XX EPI73887-A.

XX 12-MAR-1986.

PF 10-AUG-1985; 85EP-0110061.

PR 27-AUG-1984; 84JP-0179105.

PA (SHIO ) SHIONOGI KK.

PI Teraoka H, Sato K, Tanaka K;

DR WPI; 1986-070431/11.

DR N-PSDB; AAN60236.

PT New interferon alpha S51B10 and alpha S17H9 - prepd. by DNA

XX recombinant techniques

PS Claim 1; Fig 2; 37pp; English.

XX IFN alpha-S51B10 and IFN alpha-S17H9 have antiviral and antitumour  
 CC activities. Dosage is 1,000,000 - 10,000,000 units per day. IFNs are  
 CC prepared from Ball-1 cells induced with Sendai virus by known  
 CC recombinant DNA techniques.

SQ Sequence 166 AA;

Query Match 100.0%; Score 42; DB 7; Length 166;

Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTKKXSP 8  
 |||||  
 DB 131 ltkkxsp 138

Search completed: January 15, 2002, 08:40:02  
 Job time: 324 sec

Script started on Tue Jan 15 10:27:05 2002

stic10% m pir.find  
! FINDPATTERNS on pir: \* allowing 0 mismatches

1 L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)(P,R,D,L)

OXCKP2 ck: 4180 len: 724 ! acyl-CoA oxidase (EC 1.3.3.6) PXP2, peroxis

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(R)(D)(S)(N)(H)(D)(L)  
LRDSRHSL

250: TFIVP

OXCKX4 ck: 4824 len: 709 ! acyl-CoA oxidase (EC 1.3.3.6) POX4, peroxis

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(R)(D)(S)(N)(H)(D)(L)  
LRDSNHDL

228: TFVVP

OXCKAX ck: 6643 len: 502 ! acyl-CoA oxidase (EC 1.3.3.6) POX4-2, perox

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(R)(D)(S)(N)(H)(D)(L)  
LRDSNHDL

21: TFVVP

OXCKX ck: 2978 len: 709 ! acyl-CoA oxidase (EC 1.3.3.6) AOX, peroxis

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(R)(D)(S)(N)(H)(D)(L)  
LRDSNHDL

228: TFVVP

OXCKPM ck: 8367 len: 709 ! acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxis

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(R)(D)(S)(N)(H)(D)(L)  
LRDSNHDL

228: TFVVP

OXCKX5 ck: 3893 len: 662 ! acyl-CoA oxidase (EC 1.3.3.6) POX5, peroxis

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(R)(D)(S)(N)(H)(D)(L)  
LRDSNHDL

213: TFVVP

S66044 ck: 714 len: 217 ! deoxypurine kinase (EC 2.7.1.-) yaaF - Bac

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(R)(L)(E)(Y)(D)(L)  
LRIEDYDL

186: CPVLK

A64107 ck: 3967 len: 366 ! DNA-directed DNA polymerase (EC 2.7.7.7) II

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)  
L(Q)(L)(E)(D)(Y)(R)(L)  
LOIEDYRL

35: LNNVL

RRNZ42 ck: 6550 len: 2,165 ! genome polyprotein - human respiratory sync

[7m-More--(2%)] m [kstic10%

stic10%

stic10% tail pir.find

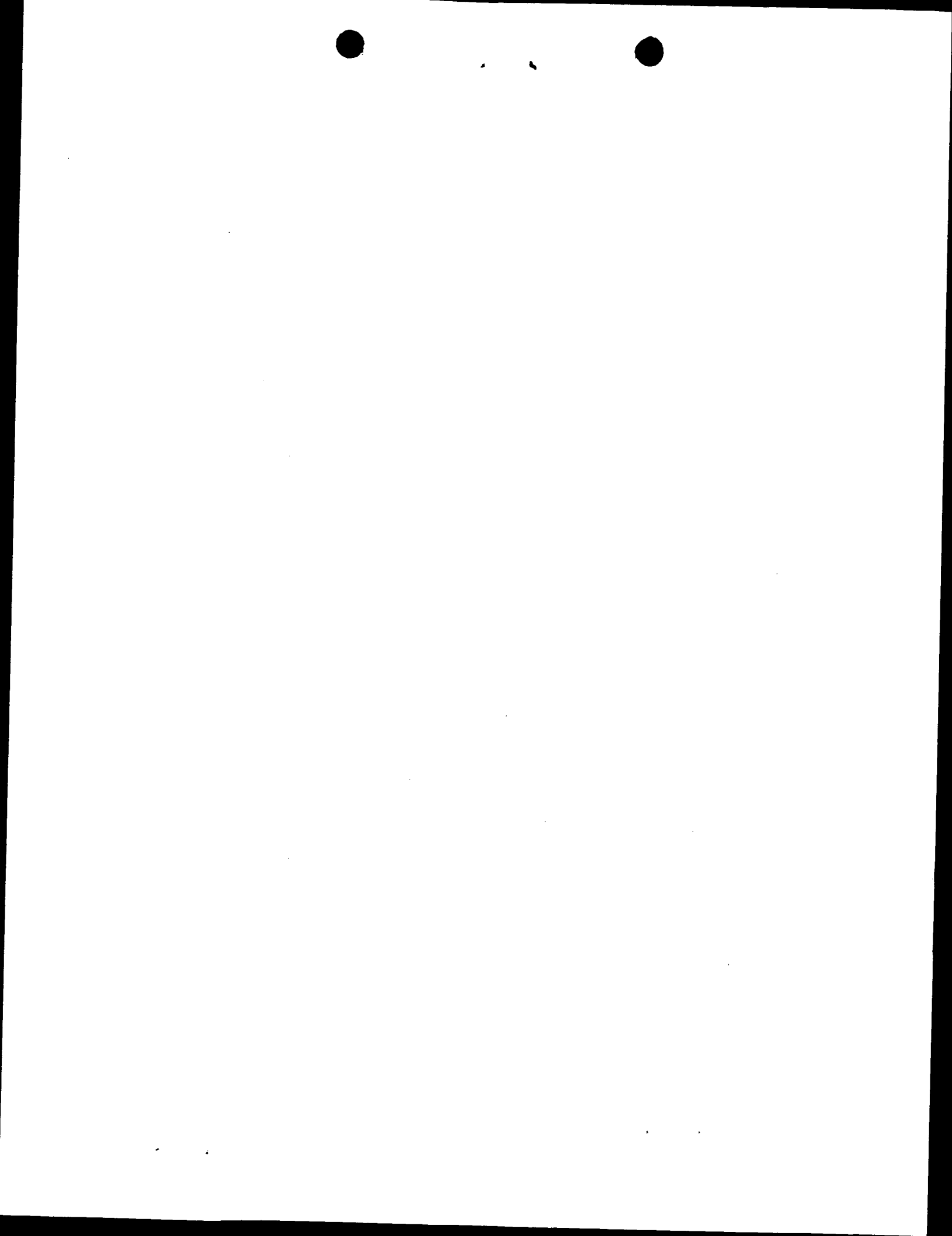
.find

Databases searched:

NBRF, Release 68.0, Released on 31Mar2001, Formatted on 26Jun2001

Total finds: 344  
Total length: 76,174,552  
Total sequences: 219,241  
CPU time: 04:37.90

stic10%  
script done on Tue Jan 15 10:27:24 2002



Script started on Tue Jan 15 10:31:55 2002

stic10% m swp.find

! FINDPATTERNS on swp: \* allowing 0 mismatches

1 L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)(P,R,D,L)

ACTR\_CAVPO ck: 5058 len: 297 1 Q92159 cavia porcellus (guinea pig) . adrenc

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)

198: YVHMF

L(M)(A)(R)(S)(H)(A)(R)

LMARSHAR

AIDA\_ECOLI ck: 8339 len: 1,286 1 Q03155 escherichia coli . adhesin aida-i pre

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)

L(E)(E)(K)(Y)(N)(L)

LEEEKYNL

1,118: VKGCG

AMY\_BUTFI ck: 4687 len: 976 1 P30269 butyrivibrio fibrisolvens . alpha-amy

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)

L(M)(I)(E)(R)(Y)(N)(D)

LMIERYND

540: GNIGT

APE2\_AERPE ck: 3114 len: 167 1 O73943 aeropyrum pernix . homing endonuclease

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)

L(T)(R)(M)(K)(Y)(R)(R)

LTRMKYRR

112: EIVLT

ASO\_CUCPM ck: 1447 len: 552 1 P37064 cucurbita pepo var. melopepo (zucchi

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)

L(G)(A)(M)(K)(Y)(N)(L)

LGAMKYNL

377: PPTPY

BIOB\_SCHPO ck: 8853 len: 363 1 O59778 schizosaccharomyces pombe (fission y

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)

L(G)(E)(K)(K)(H)(D)(R)

LGKKKHDR

213: GGILG

BUD6\_YEAST ck: 5257 len: 788 1 P41697 saccharomyces cerevisiae (baker's ye

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)

L(E)(A)(N)(K)(H)(D)(L)

LEANKHDL

489: LPQPG

CANE\_DROME ck: 2829 len: 1,507 1 Q24298 drosophila melanogaster (fruit fly)

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)

L(Q)(A)(N)(D)(Y)(D)(D)

LQANDIDD

753: GHVVO

CAOI\_CANFR ck: 2901 len: 661 1 P08790 candida tropicalis (yeast) . acyl-coe

L(T,R,Q,M,E,G)(E,R,D,L,I,A)(K,R,N,M,S,E)(K,R,D,N,S)(Y,H)(S,R,D,N,A)

L(Q)(A)(N)(D)(Y)(D)(D)

LQANDIDD

[7m--More--(1%)] m [stic10%

stic10%

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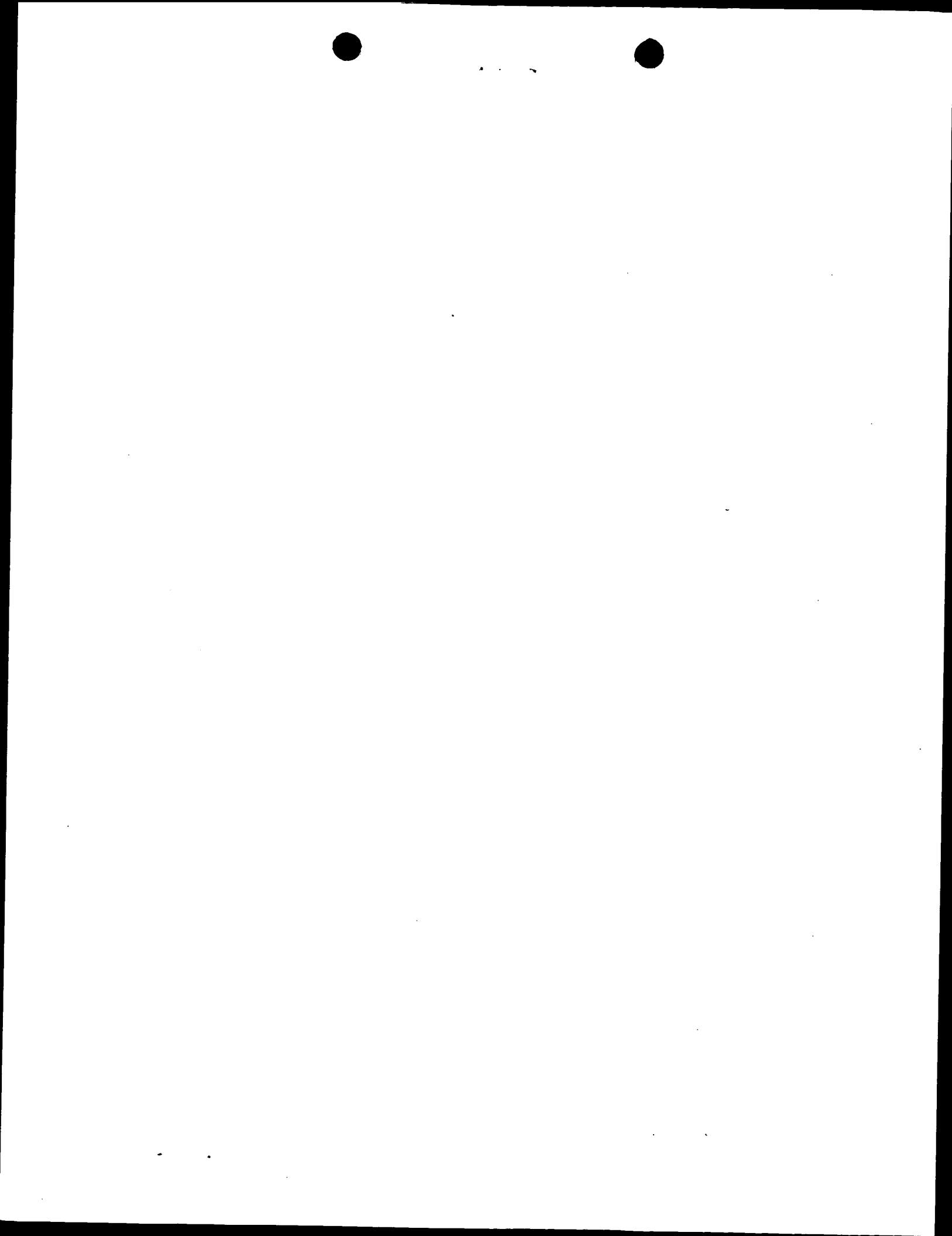
stic10%

Total finds: 654  
Total length: 182,937,156  
Total sequences: 573,564  
CPU time: 11:27.72

stic10%  
script done on Tue Jan 15 10:32:11 2002

Databases searched:

SWISS-PROT, Release 39.2, Released on 24Aug2001, Formatted on 27Aug2001  
SPTREMBL, Release 17.0, Released on 1Jun2001, Formatted on 26Jun2001





Script started on Tue Jan 15 10:32:38 2002

stic10% m agen.res

> 0 < Intelligences

> 0 <

Quest - Quick User-directed Expression Search Tool  
Release 5.4

-- Outline of search "agen" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence. "09-424080.key":

Selected sequence key from "seq2 AA preliminary pattern

```
1 followed by
2 1
2 t or r or g or m or e or g
2 e or r or d or l or i or a
2 k or r or n or m or s or e
2 k or r or d or n or s
2 y or h
2 s or r or d or n or a
2 p or r or d or l
```

Selected data banks and files:

Data bank : A-Geneseq 35.2, all entries

-- Output Parameters --

Format Options:	File Options:	Yes
Nucleic acid code matching	Exact	No
Find non-matching hits only	Indirect file	No
Report key used	Sequence or key file	No
Note position of hit	List of hits	No
Display full annotations	Hit display	Yes
Sequence context	Name and annotations	Yes

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	NO

1 match found in sequence:

P90186 : Hybrid alpha-interferon.

(from "A-Geneseq 35.2")

P90186 standard; peptide: 166 AA.

AC P90186;

DE 14-DEC-1989 (first entry)

DT Hybrid alpha-interferon.

KW Hybrid; alpha-interferon; alpha-D gene; alpha-B gene; muramylpeptide;

KW human; synthetic; herpes simplex virus 1 and 2; tumours; Lewis lung

KW carcinoma; B16-B16 melanoma; synergistic.

OS Synthetic.

FH Key

FT region

FT region

FT region

FT region

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FT region

CC Hybrid alpha-interferon consisting of 4 fragments of human  
CC lymphoblastoid or leukocyte interferons-alpha-B and -alpha-D. This is  
CC hybrid B16D3B4 which correspond, in order, to the regions specified  
CC starting with B1 (amino acids 1-60 of interferon-alpha-B). The hybrids  
CC (P90185-90) act synergistically, in a compsn. with muramyl peptide, to  
CC treat virus infections in human and veterinary medicine esp. herpes  
CC simplex virus 1 and 2. They also reduce development of metastases from  
CC some tumours, eg B16-B16 melanoma or Lewis lung carcinoma.

SO Sequence 166 AA:  
SQ 11 A: 11 R: 5 N: 11 D: 0 B: 4 C: 12 Q: 15 E: 0 Z: 2 G: 3 H:  
SQ 9 I: 21 L: 11 K: 5 M: 10 F: 5 P: 13 S: 7 T: 1 W: 4 Y: 6 V:  
Found using 'seq2' (09-424080.key)

106 vgetplmadslavkkyfrirtilyltekkyspcawevvraeimsfsinlqkrlk  
131 138

1 match found in sequence:

P90188 : Hybrid alpha-interferon.

(from "A-Geneseq 35.2")

ID P90188 standard; peptide: 166 AA.

AC P90188;

DE 14-DEC-1989 (first entry)

DT Hybrid alpha-interferon.

KW Hybrid; alpha-interferon; alpha-D gene; alpha-B gene; muramylpeptide;

KW human; synthetic; herpes simplex virus 1 and 2; tumours; Lewis lung

KW carcinoma; B16-B16 melanoma; synergistic.

OS Synthetic.

FH Key

FT region

FT region

FT region

FT region

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FT region

FT region

FT region

FT region

FT region

FT region

106 vgetplmadslavkkyfrirtilyltekkyspcawevvraeimsfsinlqkrlk  
131 138

1 match found in sequence:  
P90189 : Hybrid alpha-interferon.  
(from "A-Geneseq 35.2")

ID P90189 standard; peptide; 166 AA.  
 AC P90189;  
 DT 14-DEC-1989 (first entry)  
 DE Hybrid alpha-interferon.  
 KW human; synthetic; herpes simplex virus 1 and 2; tumours; Lewis lung carcinoma; B16-B16 melanoma; synergistic.  
 OS Synthetic.  
 FH Key  
 FT region 1..60 Location/Qualifiers  
 FT region 61..92  
 FT region 93..150  
 FT region 151..166  
 PN EP-329609-A.  
 PD 23-AUG-1989.  
 PF 06-FEB-1989; 810100.  
 PR 13-FEB-1988; GB-003365.  
 PA (CIBA) Ciba Geigy AG.  
 PI Gangeml JD, Hockkepel HK;  
 DR WPI: 89-243490/34.  
 PT Synergistic antiviral compn. - contg. hybrid alpha interferon  
 PS and muramyl peptide esp. active against herpes simplex.  
 PS Disclosure; page 3; 13pp; English.  
 CC Hybrid alpha-interferon consisting of 4 fragments of human lymphoblastoid or leukocyte interferons-alpha-B and -alpha-D. This is hybrid B12D3D4 which correspond, in order, to the regions specified starting with B1 (amino acids 1-60 of interferon-alpha-B). The hybrids (P90185-90) act synergistically, in a compn. with muramyl peptide, to treat virus infections in human and veterinary medicine, esp. herpes simplex virus 1 and 2. They also reduce development of metastases from some tumours, eg B16-B16 melanoma or Lewis lung carcinoma.  
 SO Sequence 166 AA.  
 SQ 11 A; 13 R; 5 N; 11 D; 0 B; 6 C; 12 Q; 15 E; 0 Z; 2 G; 3 H; 8 I; 21 L; 9 K; 5 M; 9 F; 5 P; 11 S; 8 T; 2 W; 4 Y; 6 V;  
 SQ found using 'seq2' (09-424080.key)  
 .....  
 106 vgetplmadslavkkyfrilylekkykspcawevraeimsislstnlqrlr  
 131 138  
 [7m--More--(2%) [m ... [K  
 -----  
 1 match found in sequence:  
 P90398 ; Feline Interferon  
 (from "A-Geneseg 35.2")  
 ID P90398 standard; protein; 171 AA.  
 AC P90398;  
 DT 1-NOV-1989 (first entry)  
 DE Feline Interferon  
 KW Feline Interferon; peptide; antiviral agent; antitumour agent.  
 OS Feline  
 PN EP-322870-A.  
 PD 05-JUL-1987.  
 PF 27-DEC-1988; 121737.  
 PR 29-DEC-1987; JP-336297.  
 PA (TORA) Toray Industries Inc.  
 PI Yanai A, Nakamura N, Matsuda S;  
 DR WPI: 89-194216/27.  
 N-PSDB; N90185.  
 PT Feline Interferon gene, protein and precursor - used for obtaining  
 PS Claim 32; page 10 and fig 7; 18pp; English.  
 CC The sequence is the peptide derived from the feline interferon gene (see N90185). The peptide may have an attached sugar chain.  
 CC Feline Interferon can be used as an antiviral and antitumour agent for cats. It may be used to treat, eg FIVV, feline leukaemia, CC feline viral rhinotracheitis, feline calicivirus disease and CC feline infectious peritonitis. When not carrying a sugar chain, CC the interferon has specific activity greater than 100000000 U/mg at 40 mol. wt. 20000 (suitable host cell is E.coli K12). With a

CC sugar chain, it has same activity and mol. wt. 24000 (suitable  
 CC host cells are COS 1, COS 7 and COS-DUK-XB-1).  
 CC See also N90186 and P90399.  
 SO Sequence 171 AA;  
 SQ 13 A; 13 R; 6 N; 8 D; 0 B; 6 C; 12 Q; 14 E; 0 Z; 6 G; 5 H; 5 I; 22 L; 7 K; 2 M; 8 F; 6 P; 14 S; 10 T; 2 W; 5 Y; 7 V;  
 SQ found using 'seq2' (09-424080.key)  
 .....  
 110 apltnedhpedsilrnyfgrlslylqekkykspcawevraeimsrlystslqkrl  
 135 142  
 -----  
 1 match found in sequence:  
 P90399 ; Feline Interferon  
 (from "A-Geneseg 35.2")  
 ID P90399 standard; protein; 194 AA.  
 AC P90399;  
 DT 1-NOV-1989 (first entry)  
 DE Feline Interferon  
 KW Feline Interferon; peptide; antiviral agent; antitumour agent.  
 OS Feline  
 PN EP-322870-A.  
 PD 05-JUL-1989.  
 PF 27-DEC-1988; 121737.  
 PR 29-DEC-1987; JP-336297.  
 PA (TORA) Toray Industries Inc.  
 PI Yanai A, Nakamura N, Matsuda S;  
 DR WPI: 89-194216/27.  
 N-PSDB; N90186.  
 PT Feline Interferon gene, protein and precursor - used for obtaining  
 PS Claim 37; page 10 and fig 8; 18pp; English.  
 CC The sequence is the peptide sequence of feline interferon precursor gene (see N90186). See also N90185 and P90398.  
 SO Sequence 194 AA;  
 SQ 16 A; 13 R; 7 N; 8 D; 0 B; 8 C; 12 Q; 14 E; 0 Z; 8 G; 5 H; 5 I; 27 L; 7 K; 3 M; 9 F; 7 P; 18 S; 10 T; 2 W; 5 Y; 10 V;  
 SQ found using 'seq2' (09-424080.key)  
 .....  
 133 apltnedhpedsilrnyfgrlslylqekkykspcawevraeimsrlystslqkrl  
 158 165  
 -----  
 1 match found in sequence:  
 P80046 ; Sequence of human Interferon alpha-1 (huIFN alpha-1) encoded on  
 (from "A-Geneseg 35.2")  
 ID P80046 standard; protein; 167 AA.  
 AC P80046;  
 DT 17-NOV-1990 (first entry)  
 DE Sequence of human Interferon alpha-1 (huIFN alpha-1) encoded on  
 KW HindIII/EcoRI fragment of pgW5  
 KW Alpha-beta hybrid interferon; multi-class hybrid interferon;  
 OS antitumour; antiviral; therapy.  
 PN Homo sapiens.  
 PN USA4758428-A.  
 PD 19-JUL-1988.  
 PF 15-JUL-1985; 755265.  
 PR 19-JAN-1983; CA-419758.  
 PA (CERTU) Cetus Corp.  
 PI Mark DF, Creasey AA;  
 DR WPI: 88-219882/31.  
 N-PSDB; n80043.

```

PF Multi-class hybrid interferon polypeptide(s)
PT having sequence from interferon-alpha-1 and sequence from
PS interferon-beta-1 for restricted activity
PS Example: Fig 3: 24pp: English.
CC Multi-class hybrid IFN polypeptides having an AA sequence composed
CC of 2 distinct subsequences are claimed. The plasmids used in the
CC construction of the huIFN alpha-1-beta-1 hybrid 1 are plasmids pGWS and
CC pDM101/trp/beta-1 contg. the genes coding for huIFN alpha-1 and huIFN
CC beta-1 respectively. The plasmid pGWS was constructed from the plasmid
CC pBR322 by substituting region between the EcoRI site to the PvuII site
CC with the E.coli trp promoter and the DNA sequence coding for the mature
CC protein of huIFN alpha-1.
SQ Sequence 167 AA:
SQ 8 A; 12 R; 6 N; 11 D; 0 B; 5 C; 10 Q; 16 E; 0 Z; 3 G; 3 H;
SQ 6 I; 22 L; 8 K; 8 M; 8 F; 6 P; 13 S; 9 T; 2 W; 4 Y; 7 V;
Found using 'seq2' (09-424080.key)

```

```

17m--More--(3%) [m 107
|-----|
132 139
vegtpimvdsilavkkyfrritlyltekkywpcawevraeimsrslstnlgelr

```

1 match found in sequence:

```

P80052 : Sequence of human interferon (huIFN) alpha-61A gene in p-alpha-61A
(from "A-Geneseg 35.2")
ID P80052 standard; protein: 167 AA.

```

```

AC P80052;
DT 17-NOV-1990 (first entry)
DE Sequence of human interferon (huIFN) alpha-61A gene in p-alpha-61A
KW Alpha-beta hybrid interferon; multi-class hybrid interferon;
KW antitumor; antiviral; therapy.
OS Homo sapiens.
PN US4758428-A.
PD 19-JUL-1988.
PF 15-JUL-1985; 755265.
PR 19-JAN-1983; CA-419758.
PR 15-JUL-1985; US-755265,
PA (CETR) Celus Corp.
PI Mark DF, Creasey AA;
DR WPI; 88-219882/31.
DR N-PSDB: n80049.
PT Multi-class hybrid interferon polypeptide(s)
PT having sequence from interferon-alpha-1 and sequence from
PT interferon-beta-1 for restricted activity
PS Example: Fig 16: 24pp: English.
CC Multi-class hybrid interferon polypeptides having an AA sequence composed
CC of 2 distinct subsequences are claimed. The plasmids used in the
CC construction of huIFN-alpha-61A-beta-1 hybrid are plasmids palpha61A and
CC pDM101/trp/beta-1. Assembly of the palpha61A plasmid involved replacing
CC the DNA fragment encoding the 23 AA signal polypeptide of preinterferon
CC with a 120bp EcoRI/Sau3A promoter fragment E.coli trp promoter, operator,
CC and trp leader ribosome binding site preoperator, encoding an ATG
CC initiation codon and using HindIII site that was inserted, 59 nucleotides
CC 3'-end of the TGA translational stop codon, to insert the gene into the
CC plasmid pBR11 (a deriv of pBR322 having a deletion between the HindIII
CC and PvuII sites). The complete DNA sequence of the promoter and gene
CC fragments inserted between the EcoRI and HindIII sites of pBR11 is shown
CC in n80049.
SQ Sequence 167 AA:
SQ 8 A; 11 R; 6 N; 9 D; 0 B; 3 C; 13 Q; 13 E; 0 Z; 4 G; 4 H;
SQ 7 I; 18 L; 8 K; 9 M; 10 F; 5 P; 14 S; 11 T; 2 W; 5 Y; 7 V;
Found using 'seq2' (09-424080.key)

```

```

107 vedtpimvdsilavkkyfrritlyltekkywpcawevraeimsrslstnlgelr
132 139

```

1 match found in sequence:

```

P80051 : Sequence of human interferon (huIFN)-beta-1 alpha-1 hybrid 1
(from "A-Geneseg 35.2")
ID P80051 standard; protein: 167 AA.

```

```

AC P80051;
DT 17-NOV-1990 (first entry)
DR 17m--More--(4%) [m [stic10%
stic10%
stic10%

```

stic10% tail agen.res

-- Search Statistics --

```

Times: CPU Total Elapsed
00:00:40.09 00:01:18.00

```

```

Number of sequences searched: 170751
Number of sequence hits: 153
Number of separate matches: 153
Number of sequence hits saved: 0

```

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stic10%
script done on Tue Jan 15 10:33:02 2002

```



Script started on Tue Jan 15 10:39:04 2002

stic10% m pen.res

> 0 <  
0110 Intelligentics

Quest - Quick User-directed Expression Search Tool  
Release 5.4

-- Outline of search "pen" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence "09-424080.key":

Selected sequence key from "09-424080.key":  
seq2 (AA) ID seq2 AA preliminary pattern

followed by  
1 t o r r o r q o r m o r e o r g  
2 e o r r o r d o r l o r i o r a  
2 k o r r o r n o r m o r s o r e  
2 k o r r o r d o r n o r s  
2 y o r h  
2 s o r r o r d o r n o r a  
2 p o r r o r d o r l

Selected data banks and files:

Data bank : Pending\_AA , all entries

-- Output Parameters --

Format Options:	File Options:
Nucleic acid code matching	Exact
Find non-matching hits only	No
Report key used	Yes
Note position of hit	Yes
Display full annotations	Yes
Sequence context	25

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	No

1 match found in sequence:

PCT-US00-01239-8 ; Sequence 8, Application PC/TUS0001239  
(from "/srch/paa/PCTUS\_COMB.pep")  
Sequence 8, Application PC/TUS0001239

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Keratinocyte Derived Interferon

FILE REFERENCE: PP482PI

CURRENT APPLICATION NUMBER: PCT/US00/01239

CURRENT FILING DATE: 2000-01-20

EARLIER APPLICATION NUMBER: 60/093,643

EARLIER FILING DATE: 1998-07-21

EARLIER APPLICATION NUMBER: PCT/US99/16424

EARLIER FILING DATE: 1999-07-21

NUMBER OF SEQ ID NOS: 54

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 8

17m--More--(0%) 1m LENGTH: 189

TYPE: PRT

ORGANISM: Homo sapiens

Found using 'seq2' (09-424080.key)

154 161

1 match found in sequence:

PCT-US00-05881-828 ; Sequence 828, Application PC/TUS0005881  
(from "/srch/paa/PCTUS\_COMB.pep")  
Sequence 828, Application PC/TUS0005881

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

APPLICANT: Steve Ruden

TITLE OF INVENTION: Human Breast and Ovarian Cancer Associated Gene Sequences and P

FILE REFERENCE: PA103PCT

CURRENT APPLICATION NUMBER: PCT/US00/05881

CURRENT FILING DATE: 2000-03-08

EARLIER APPLICATION NUMBER: 60/124,270

EARLIER FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 846

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 828

LENGTH: 78

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (43)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (56)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Found using 'seq2' (09-424080.key)

1 LVFTETLREHKFMGLMILLGIMSYSSLSLNNVKKHCSQRXLLSTAINHG  
21 28

1 match found in sequence:

PCT-US00-05988-1444 ; Sequence 1444, Application PC/TUS0005988  
(from "/srch/paa/PCTUS\_COMB.pep")  
Sequence 1444, Application PC/TUS0005988

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

APPLICANT: Steve Ruden

TITLE OF INVENTION: Human Prostate Cancer Associated Gene Sequences and Polypeptide

FILE REFERENCE: PA101PCT

CURRENT APPLICATION NUMBER: PCT/US00/05988

CURRENT FILING DATE: 2000-03-08

EARLIER APPLICATION NUMBER: 60/124,270

EARLIER FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1444

LENGTH: 531

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (6)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (446)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (474)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE  
 LOCATION: (502)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 FEATURE:  
 NAME/KEY: SITE  
 LOCATION: (504)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 Found using 'seq2' (09-424080.key)

16 SPSPEIYNSGKRLNREFFTRKKLEDEHNLITEMVALNPDKPPADKKPATRYS  
 41 48

match found in sequence:  
 PCT-US00-07285-106 ; Sequence 106, Application PC/TUS0007285  
 (from "/srch/paa/pcrus\_comb.pep")  
 Sequence 106, Application PC/TUS0007285  
 GENERAL INFORMATION:  
 APPLICANT: Valenzuela, Dario  
 APPLICANT: Yuan, Olive  
 APPLICANT: Hoffman, Heidi  
 APPLICANT: Hall, Jeff  
 APPLICANT: Rapielko, Peter

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
 \* FILE REFERENCE: GI 6919X  
 CURRENT APPLICATION NUMBER: PCT/US00/07285  
 CURRENT FILING DATE: 2000-03-17  
 NUMBER OF SEQ ID NOS: 194  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 106  
 LENGTH: 431  
 TYPE: PRT

ORGANISM: Homo sapiens  
 Found using 'seq2' (09-424080.key)  
 [7m-More--(0%) [m ... [k

387 IGLLEGVLFVLTGLVLLGRILSELRRKRSRLDYINGIYVDI  
 412 419

match found in sequence:  
 PCT-US00-08982-108 ; Sequence 108, Application PC/TUS0008982  
 (from "/srch/paa/pcrus\_comb.pep")  
 Sequence 108, Application PC/TUS0008982  
 GENERAL INFORMATION:  
 APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: 48 Human Secreted Proteins  
 FILE REFERENCE: PS542PCT  
 CURRENT APPLICATION NUMBER: PCT/US00/08982  
 CURRENT FILING DATE: 2000-04-06  
 EARLIER APPLICATION NUMBER: 60/128,696  
 EARLIER FILING DATE: 1999-04-09  
 EARLIER APPLICATION NUMBER: 60/176,069  
 EARLIER FILING DATE: 2000-01-14  
 NUMBER OF SEQ ID NOS: 142  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 108  
 LENGTH: 66  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 Found using 'seq2' (09-424080.key)

1 LSPRLGSGAISAHCKRLRLTDSRHSPPASACSWDYRRPPRRGQLSVFSVEM  
 19 26

1 match found in sequence:  
 PCT-US00-08983-141 ; Sequence 141, Application PC/TUS0008983  
 (from "/srch/paa/pcrus\_comb.pep")  
 Sequence 141, Application PC/TUS0008983  
 GENERAL INFORMATION:  
 APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: 50 Human Secreted Proteins  
 FILE REFERENCE: PS543PCT  
 CURRENT APPLICATION NUMBER: PCT/US00/08983  
 CURRENT FILING DATE: 2000-04-06  
 EARLIER APPLICATION NUMBER: 60/128,703  
 EARLIER FILING DATE: 1999-04-09  
 EARLIER APPLICATION NUMBER: 60/176,068  
 EARLIER FILING DATE: 2000-01-20  
 NUMBER OF SEQ ID NOS: 152  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 141  
 LENGTH: 372  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 Found using 'seq2' (09-424080.key)

75 SSSSLASGEFTGVKELDISQETIAQLQRRKSLLEODIREKEAIRKQTSVEQELQNDL  
 [7m-More--(0%) [m 100 107

1 match found in sequence:  
 PCT-US00-08983-142 ; Sequence 142, Application PC/TUS0008983  
 (from "/srch/paa/pcrus\_comb.pep")  
 Sequence 142, Application PC/TUS0008983  
 GENERAL INFORMATION:  
 APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: 50 Human Secreted Proteins  
 FILE REFERENCE: PS543PCT  
 CURRENT APPLICATION NUMBER: PCT/US00/08983  
 CURRENT FILING DATE: 2000-04-06  
 EARLIER APPLICATION NUMBER: 60/128,703  
 EARLIER FILING DATE: 1999-04-09  
 EARLIER APPLICATION NUMBER: 60/176,068  
 EARLIER FILING DATE: 2000-01-20  
 NUMBER OF SEQ ID NOS: 152  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 142  
 LENGTH: 371  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 NAME/KEY: SITE  
 LOCATION: (370)  
 OTHER INFORMATION: Xaa equals stop translation  
 Found using 'seq2' (09-424080.key)

75 SSGSLASGEFTGVKELDISQETIAQLQREKSLLEODIREKEAIRKQTSVEQELQNDL  
 100 107

1 match found in sequence:  
 PCT-US00-26524B-6953 ; Sequence 6953, Application PC/TUS0026524B  
 (from "/srch/paa/pcrus\_comb.pep")  
 Sequence 6953, Application PC/TUS0026524B

## GENERAL INFORMATION:

APPLICANT: Birse et. al.  
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides

FILE REFERENCE: PA005PCT  
CURRENT APPLICATION NUMBER: PCT/US00/26524B

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: 60/157,137

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/163,280

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 6953

LENGTH: 92

TYPE: PRT

ORGANISM: Homo sapiens

Found using 'seq2' (09-424080.key)

(7m--More--(0%)) [m [K

...

NOFKEMFLYKTPENSIOEEREAAILRLSKYSKGCPRMAYMFGWQVDSITSPASLH

58 65

## 1 match found in sequence:

PCT-US01-35017A-1414 ; Sequence 1414, Application PC/TUS0035017A

(from "/src/paa/PCTUS\_COMB.pep")

Sequence 1414, Application PC/TUS0035017A

GENERAL INFORMATION:

APPLICANT: Hyseq Inc

TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

FILE REFERENCE: 784PCT

CURRENT APPLICATION NUMBER: PCT/US00/35017A

CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US09/488,725

PRIOR FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US09/552,317

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 1478

SEQ ID NO 1414

LENGTH: 365

TYPE: PRT

ORGANISM: Homo sapiens

Found using 'seq2' (09-424080.key)

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IGSLFGLVFLVIGLVGLRILSESRARRKRSRLDYLINGIYVDI

346 353

## 1 match found in sequence:

PCT-US01-00663-28110 ; Sequence 28110, Application PC/TUS0100663

(from "/src/paa/PCTUS\_COMB.pep")

Sequence 28110, Application PC/TUS0100663

GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: PB 0004 WO 7

CURRENT APPLICATION NUMBER: PCT/US01/00663

CURRENT FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 26 May 2000 (26.05.00)

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 03 October 2000 (03.10.00)

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 38837

SOFTWARE: Molecular Dynamics Sequence Listing Engine

SEQ ID NO 28110

LENGTH: 47

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: MAP TO AC009363.3

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6.9

OTHER INFORMATION: EST\_HUMAN HIT: BE906024.1, EVALUATE 1.00e-19

OTHER INFORMATION: SWISSPROT HIT: Q60765, EVALUATE 8.00e-13

Found using 'seq2' (09-424080.key)

...

ERLELMAELKTOLEELKQEROOLILMLNRHPTCTVTRDSVKT

28 35

## 1 match found in sequence:

PCT-US01-00663-31537 ; Sequence 31537, Application PC/TUS0100663

(from "/src/paa/PCTUS\_COMB.pep")

Sequence 31537, Application PC/TUS0100663

GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: PB 0004 WO 7

CURRENT APPLICATION NUMBER: PCT/US01/00663

CURRENT FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 26 May 2000 (26.05.00)

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 03 August 2000 (03.08.00)

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PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 38837

SOFTWARE: Molecular Dynamics Sequence Listing Engine

SEQ ID NO 31537

LENGTH: 751

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: MAP TO AL049872.3

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7

OTHER INFORMATION: EST\_HUMAN HIT: A0138211.1, EVALUATE 2.00e-83

OTHER INFORMATION: SWISSPROT HIT: Q10411, EVALUATE 3.00e-18

Found using 'seq2' (09-424080.key)

572 SSELLOEELKSLQEKDATTITLOENNRHSDSIAATSELERKEHQDTSEIKOL  
597 564

1 match found in sequence:

PCT-US01-00663-34035 : Sequence 34035, Application PC/TUS0100663  
(from "/srch/paa/PC/TUS-COMB.pep")

Sequence 34035, Application PC/TUS0100663

GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: PB 0004 WO 7

CURRENT APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR FILING DATE: 26 May 2000 (26.05.00)

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR FILING DATE: 03 October 2000 (03.10.00)

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 38837

SOFTWARE: Molecular Dynamics Sequence Listing Engine

SEQ ID NO 34035

LENGTH: 75

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AC004614.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2

OTHER INFORMATION: SWISSPROT HIT: P45702, EVALU 1.80e+00

OTHER INFORMATION: EST HUMAN HIT: AA249238.1, EVALU 6.60e-01

Found using 'seq2' (09-424080.key)

[7m--More--(0%) [m 11 TEIMSSMKKEGRIKNGLEKMLALRIIRRHAPGICGWRPKNMGTKRAKALRIAIVY  
36 43

1 match found in sequence:

PCT-US01-00663-34955 : Sequence 34955, Application PC/TUS0100663  
(from "/srch/paa/PC/TUS-COMB.pep")

Sequence 34955, Application PC/TUS0100663

GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: PB 0004 WO 7

CURRENT APPLICATION NUMBER: PCT/US01/00663

CURRENT FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 26 May 2000 (26.05.00)

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 03 October 2000 (03.10.00)

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 38837

SOFTWARE: Molecular Dynamics Sequence Listing Engine

SEQ ID NO 34955

LENGTH: 69

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AL133229.19

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4

OTHER INFORMATION: SWISSPROT HIT: P16543, EVALU 3.40e+00

Found using 'seq2' (09-424080.key)

1 MGATAPAAVAGYIRGCGVPAISLEASHRLILNSSTENRGNRSALVLRMTLVRT

25 32

1 match found in sequence:

PCT-US01-00663-38470 : Sequence 38470, Application PC/TUS0100663  
(from "/srch/paa/PC/TUS-COMB.pep")

Sequence 38470, Application PC/TUS0100663

GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.

APPLICANT: Penn, Sharon G.

[7m--More--(0%) [m [kstic10%

stic10%

stic10% tail pen.res

Times: -- Search Statistics --

CPU 00:23:34.02

Number of sequences searched: 3293760

Number of sequence hits: 1411

Number of separate matches: 1413

Number of sequence hits saved: 0

stic10%

script done on Tue Jan 15 10:39:19 2002

Total Elapsed 00:31:00.00



Found using 'seq2' (09-424080.key)

25 DPYANPLSDVMSRLAKVKDLTPGELTAESYDSDYLDDEDADMTATGOGOKSAGDTSF  
50 57

1 match found in sequence:  
US-08-286-888B-6; Sequence 6, Application US/0828688B  
(from "/srch/laa/5A.COMB.pep")  
Sequence 6, Application US/0828688B  
Patent No. 5627024

## GENERAL INFORMATION:

APPLICANT: Maruyama, Ichiro  
APPLICANT: Maruyama, Hiroko  
APPLICANT: Brenner, Sydney  
TITLE OF INVENTION: LAMBDROID BACTERIOPHAGE VECTORS FOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESS: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5627024th Torrey Pines Road, TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,888B  
FILING DATE: 05-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 432.0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312

[7m--More--(3\*)]m  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 292 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: peptide  
LOCATION: 177  
OTHER INFORMATION: /label= Xaa  
OTHER INFORMATION: /note= "Wherein Xaa is a suppressor termination  
Found using seq2' (09-424080.key)

25 DPYANPLSDVMSRLAKVKDLTPGELTAESYDSDYLDDEDADMTATGOGOKSAGDTSF  
50 57

## 1 match found in sequence:

US-08-294-386C-1; Sequence 1, Application US/08294386C  
(from "/srch/laa/5A.COMB.pep")  
Sequence 1, Application US/08294386C  
Patent No. 5646030  
GENERAL INFORMATION:  
APPLICANT: Ray, Bryan L.

APPLICANT: Lin, Edmund C.C.  
APPLICANT: Crea, Roberto  
TITLE OF INVENTION: Method Of Isolating Mutant Cells  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESS: Lappin & Kusmer  
STREET: 200 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/294,386C  
FILING DATE: August 23, 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: SYZ-010CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/330-1300  
TELEFAX: 617/330-1311  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 246 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
Found using 'seq2' (09-424080.key)

25 DPYANPLSDVMSRLAKVKDLTPGELTAESYDSDYLDDEDADMTATGOGOKSAGDTSF  
50 57

## 1 match found in sequence:

US-08-294-386C-3; Sequence 3, Application US/08294386C  
(from "/srch/laa/5A.COMB.pep")  
Sequence 3, Application US/08294386C  
Patent No. 5646030  
GENERAL INFORMATION:

APPLICANT: Ray, Bryan L.  
APPLICANT: Lin, Edmund C.C.  
APPLICANT: Crea, Roberto  
TITLE OF INVENTION: Method Of Isolating Mutant Cells  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESS: Lappin & Kusmer  
STREET: 200 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/294,386C  
FILING DATE: August 23, 1994

CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kerner, Ann-Louise  
 REGISTRATION NUMBER: 33,523  
 REFERENCE/DOCKET NUMBER: SYZ-010CIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/330-1300  
 TELEFAX: 617/330-1311  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 246 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 Found using 'seq2' (09-424080.key)

7m--More--(5%) [m [K  
 |-----|  
 DPYANPLSDVDWMSRLAKVKDLTPGELTAESYDDSYLDDEDADMTATGGGQKSAGDTSF  
 50 57

1 match found in sequence:  
 US-08-299-249A-1; Sequence 1, Application US/08299249A

(from "/srch/laa/5A\_COMB.pep")  
 Sequence 1, Application US/08299249A  
 Patent No. 5650267

# GENERAL INFORMATION:

\* APPLICANT: RAY, Bryan L.; and  
 TITLE OF INVENTION: Method Of Detecting Compounds  
 TITLE OF INVENTION: Utilizing Genetically Modified  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HALE and DORR  
 STREET: 60 State Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: U.S.A.  
 ZIP: 02109

# COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/299,249A

FILING DATE: 31-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/053,865

FILING DATE: 27-APR-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: SYZ-011FWC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/526-6000

TELEFAX: 617/526-5000

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 246 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide  
 HYPOTHETICAL: YES  
 Found using 'seq2' (09-424080.key)

25 DPYANPLSDVDWMSRLAKVKDLTPGELTAESYDDSYLDDEDADMTATGGGQKSAGDTSF  
 |-----|  
 7m--More--(6%) [m [Kstic10%  
 stic10%  
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# -- Search Statistics --

Times:	CPU	Total Elapsed
	00:01:58.07	00:04:44.00
Number of sequences searched:		212306
Number of sequence hits:		124
Number of separate matches:		124
Number of sequence hits saved:		0

stic10%  
 script done on Tue Jan 15 10:33:31 2002

1

2

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: January 15, 2002, 08:35:33 ; Search time 19.95 Seconds

(without alignments)  
9.024 Million cell updates/sec

Title: US-09-424-080A-1

Perfect score: 42

Sequence: 1 LTRKXSP 8

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 50 summaries

## Database :

Issued Patents-AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/CTUS.COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/Dackfilest.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	8	2	US-08-669-284B-30
2	42	100.0	11	1	US-08-362-453-4
3	42	100.0	18	1	US-08-362-453-5
4	42	100.0	150	1	US-08-362-453-10
5	42	100.0	150	1	US-08-362-453-11
6	42	100.0	150	1	US-08-362-453-12
7	42	100.0	162	1	US-08-362-453-15
8	42	100.0	165	1	US-08-362-453-13
9	42	100.0	165	1	US-08-362-453-14
10	42	100.0	166	1	US-08-362-453-8
11	42	100.0	166	2	US-08-362-453-9
12	42	100.0	166	2	US-08-489-066A-16
13	42	100.0	166	3	US-08-489-072A-16
14	42	100.0	166	3	US-08-819-238A-2
15	42	100.0	166	4	US-08-954-395A-9
16	42	100.0	166	4	US-08-954-395A-11
17	42	100.0	166	4	US-08-954-395A-12
18	42	100.0	166	4	US-08-954-395A-13
19	42	100.0	166	4	US-08-954-395A-14
20	42	100.0	166	4	US-08-954-395A-15
21	42	100.0	166	4	US-08-954-395A-16
22	42	100.0	166	4	US-08-954-395A-17
23	42	100.0	166	4	US-08-954-395A-18
24	42	100.0	166	4	US-08-489-071A-16
25	42	100.0	166	4	US-09-339-913B-75
26	42	100.0	166	4	US-09-339-913B-76
27	42	100.0	166	4	US-09-339-913B-77

28	42	100.0	166	4	US-09-339-913B-79	Sequence 79, Appl
29	42	100.0	166	4	US-09-339-913B-80	Sequence 80, Appl
30	42	100.0	166	4	US-09-339-913B-83	Sequence 83, Appl
31	42	100.0	166	4	US-09-339-913B-84	Sequence 84, Appl
32	42	100.0	166	4	US-09-339-913B-85	Sequence 85, Appl
33	42	100.0	189	1	US-08-026-758-1	Sequence 1, Appl
34	42	100.0	189	1	US-08-026-758-2	Sequence 2, Appl
35	42	100.0	189	1	US-08-026-758-3	Sequence 3, Appl
36	42	100.0	189	1	US-08-026-758-6	Sequence 6, Appl
37	42	100.0	189	1	US-08-026-758-7	Sequence 7, Appl
38	42	100.0	189	1	US-08-026-758-11	Sequence 11, Appl
39	42	100.0	189	1	US-08-026-758-16	Sequence 16, Appl
40	42	100.0	189	1	US-08-026-758-17	Sequence 17, Appl
41	42	100.0	189	1	US-08-026-758-19	Sequence 19, Appl
42	42	100.0	189	1	US-08-026-758-20	Sequence 20, Appl
43	42	100.0	189	2	US-08-489-066A-2	Sequence 2, Appl
44	42	100.0	189	3	US-08-489-072A-2	Sequence 1, Appl
45	42	100.0	189	4	US-09-206-935-8	Sequence 8, Appl
46	42	100.0	189	4	US-09-206-935-10	Sequence 10, Appl
47	42	100.0	189	4	US-09-206-935-11	Sequence 11, Appl
48	42	100.0	189	4	US-09-206-935-12	Sequence 12, Appl
49	42	100.0	189	4	US-09-206-935-18	Sequence 18, Appl
50	42	100.0	189	4	US-09-206-935-19	Sequence 19, Appl

## ALIGNMENTS

RESULT 1  
US-08-669-284B-30  
; Sequence 30, Application US/08669284B  
; Patent No. 5939534  
; GENERAL INFORMATION:  
; APPLICANT: Inoue, Makoto  
; APPLICANT: Kikuchi, Kaoru  
; APPLICANT: Ishige, Yoko  
; APPLICANT: Ito, Akira  
; APPLICANT: Kimura, Toru  
; APPLICANT: Nakayama, Chikao  
; APPLICANT: No. 5939534ch1, Hiroshi  
; TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUROTROPHIC FACTORS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/669,284B  
; FILING DATE: 28-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP94/02269  
; FILING DATE: 27-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 06-268281  
; FILING DATE: 05-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 06-201504  
; FILING DATE: 02-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 05-350934  
; FILING DATE: 29-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nakamura, Dean H.  
; REGISTRATION NUMBER: 33,981  
; REFERENCE/DOCKET NUMBER: Q-42041

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-669-284B-30

Query Match 100.0%; Score 42; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
b 1 LTERKYS 8

RESULT 2  
US-08-362-453-4  
Sequence 4, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kirts, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-362-453-4

Query Match 100.0%; Score 42; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0064;  
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
Db 2 LTERKYS 9

RESULT 3  
US-08-362-453-5  
Sequence 5, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kirts, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-362-453-5

Query Match 100.0%; Score 42; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
Db 9 LTERKYS 16

RESULT 4  
US-08-362-453-10  
Sequence 10, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington

STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kiltz, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-362-453-10

Query Match 100.0%; Score 42; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTRKXSP 8  
|||||  
DB 126 LTRKXSP 133

RESULT 5  
US-08-362-453-11  
Sequence 11, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kiltz, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-362-453-11

APPLICATION NUMBER: PCT/CA93/00279  
APPLICATION NUMBER: FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kiltz, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-362-453-11

Query Match 100.0%; Score 42; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTRKXSP 8  
|||||  
DB 126 LTRKXSP 133

RESULT 6  
US-08-362-453-12  
Sequence 12, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kiltz, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-362-453-12

Query Match 100.0%; Score 42; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
Db 126 LTERKXSP 133

## RESULT 7

US-08-362-453-15  
; Sequence 15, Application US/08362453  
; Patent No. 5684129  
; GENERAL INFORMATION:  
; APPLICANT: FISH, Eleanor N.  
; TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
; STREET: 655 Fifteenth Street N.W. Suite 330  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/362,453  
; FILING DATE: 06-JAN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/909,739  
; APPLICATION NUMBER: FILING DATE: 07-JUL-1992  
; APPLICATION NUMBER: FILING DATE: 07/980,525  
; APPLICATION NUMBER: FILING DATE: 20-NOV-1992  
; APPLICATION NUMBER: PCT/CA93/00279  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kirts, Monica Chin  
; REGISTRATION NUMBER: 36,105  
; REFERENCE/DOCKET NUMBER: P638-4017  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 638-5000  
; TELEFAX: (202) 638-4810  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 162 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-362-453-15

Query Match 100.0%; Score 42; DB 1; Length 162;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
Db 127 LTERKXSP 134

## RESULT 8

US-08-362-453-13  
; Sequence 13, Application US/08362453  
; Patent No. 5684129  
; GENERAL INFORMATION:  
; APPLICANT: FISH, Eleanor N.  
; TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES

NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
APPLICATION NUMBER: FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: FILING DATE: 07/980,525  
APPLICATION NUMBER: FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
ATTORNEY/AGENT INFORMATION:  
NAME: Kirts, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 165 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-362-453-13

Query Match 100.0%; Score 42; DB 1; Length 165;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
Db 130 LTERKXSP 137

RESULT 9  
US-08-362-453-14  
; Sequence 14, Application US/08362453  
; Patent No. 5684129  
; GENERAL INFORMATION:  
; APPLICANT: FISH, Eleanor N.  
; TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
; STREET: 655 Fifteenth Street N.W. Suite 330  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/362,453  
; FILING DATE: 06-JAN-1995  
; CLASSIFICATION: 514



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
APPLICATION NUMBER: FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
APPLICATION NUMBER: FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
APPLICATION NUMBER: FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KILTS, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 165 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
08-362-453-14

Query Match 100.0%; Score 42; DB 1; Length 165;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
DB 130 LTERKXSP 137

RESULT 10  
US-08-362-453-8  
Sequence 8, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
APPLICATION NUMBER: FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
APPLICATION NUMBER: FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
APPLICATION NUMBER: FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KILTS, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids

TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-362-453-8

Query Match 100.0%; Score 42; DB 1; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
DB 131 LTERKXSP 138

RESULT 11  
US-08-362-453-9  
Sequence 9, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
APPLICATION NUMBER: FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
APPLICATION NUMBER: FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
APPLICATION NUMBER: FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KILTS, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-362-453-9

Query Match 100.0%; Score 42; DB 1; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
DB 131 LTERKXSP 138

RESULT 12  
US-08-489-066A-16

; Sequence 16, Application US/08489066A  
; Patent No. 5869293  
; GENERAL INFORMATION:  
; APPLICANT: PESTKA, SIDNEY  
; TITLE OF INVENTION: SUPER PROTEINS INCLUDING INTERFERONS,  
; TITLE OF INVENTION: INTERLEUKINS, ET AL.  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/489,066A  
; FILING DATE: 09-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/257,784  
; FILING DATE: 10-JUN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/076,231  
; FILING DATE: 11-JUN-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fehner, Ph.D., Esq., Paul F.  
; REGISTRATION NUMBER: 35,135  
; REFERENCE/DOCKET NUMBER: 1705-1-002 CIPC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 166 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; IMMEDIATE SOURCE:  
; CLONE: Hu-IFN-alpha001  
; US-08-489-066A-16

Query Match 100.0%; Score 42; DB 2; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKKSP 8  
|11111111|  
Db 131 LTERKKSP 138

RESULT 13  
US-08-489-072A-16  
; Sequence 16, Application US/08489072A  
; Patent No. 6001589  
; GENERAL INFORMATION:  
; APPLICANT: PESTKA, SIDNEY  
; TITLE OF INVENTION: SUPER PROTEINS INCLUDING INTERFERONS,  
; TITLE OF INVENTION: INTERLEUKINS, ET AL.  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack

; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/489,072A  
; FILING DATE: 09-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/257,784  
; FILING DATE: 10-JUN-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/076,231  
; FILING DATE: 11-JUN-1993  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fehner, Ph.D., Esq., Paul F.  
; REGISTRATION NUMBER: 35,135  
; REFERENCE/DOCKET NUMBER: 1705-1-002 CIPA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 166 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; IMMEDIATE SOURCE:  
; CLONE: Hu-IFN-alpha001  
; US-08-489-072A-16

Query Match 100.0%; Score 42; DB 3; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKKSP 8  
|11111111|  
Db 131 LTERKKSP 138

RESULT 14  
US-08-819-238A-2  
; Sequence 2, Application US/08819238A  
; Patent No. 6069133  
; GENERAL INFORMATION:  
; APPLICANT: Henry C. Chlou and Dennis J. Carlo  
; TITLE OF INVENTION: TARGETED DELIVERY OF GENES ENCODING  
; TITLE OF INVENTION: INTERFERON  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHYE & COCKFIELD, LLP  
; STREET: 60 STATE STREET, SUITE 510  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/819,238A  
; FILING DATE:

CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/616,023  
FILING DATE: 14 MARCH 1996  
APPLICATION NUMBER: PCT/US96/  
FILING DATE: 14 MARCH 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: REMILLARD, JANE E.  
REGISTRATION NUMBER: 38,872  
REFERENCE/DOCKET NUMBER: TTI-143CPC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: Internal  
US-08-819-238A-2

Query Match 100.0%; Score 42; DB 3; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
|||||  
Db 131 LTERKXSP 138

RESULT 15  
US-08-954-395A-9  
Sequence 9, Application US/08954395A  
Patent No. 6204022  
GENERAL INFORMATION:  
APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelle H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880

TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
LIBRARY: Genbank Accessn. J00210, PID 9386796  
CLONE: Human IFN alpha-d, mature protein  
US-08-954-395A-9

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
|||||  
Db 131 LTERKXSP 138

RESULT 16  
US-08-954-395A-10  
Sequence 10, Application US/08954395A  
Patent No. 6204022  
GENERAL INFORMATION:  
APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelle H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: HuIFN-alpha analog IFNa-N0  
US-08-954-395A-10

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
|||||||  
Db 131 LTERKXSP 138

RESULT 17  
US-08-954-395A-11  
Sequence 11, Application US/08954395A  
Patent No. 6204022

## GENERAL INFORMATION:

APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelle H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
TITLE OF INVENTION: ANALOG  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: HuIFN-alpha analog IFNa-N1  
US-08-954-395A-11

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
|||||||  
Db 131 LTERKXSP 138

RESULT 18  
US-08-954-395A-12  
Sequence 12, Application US/08954395A  
Patent No. 6204022

## GENERAL INFORMATION:

APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelle H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
TITLE OF INVENTION: ANALOG  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: HuIFN-alpha analog IFNa-N2  
US-08-954-395A-12

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
|||||||  
Db 131 LTERKXSP 138

RESULT 19  
US-08-954-395A-13  
Sequence 13, Application US/08954395A

Patent No. 6204022  
GENERAL INFORMATION:  
APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelle H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: HuIFN-alpha analog IFNa-N3  
US-08-954-395A-13

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKYSK 8  
Db 131 LTERKYSK 138

RESULT 20  
US-08-954-395A-14  
Sequence 14, Application US/08954395A  
Patent No. 6204022  
GENERAL INFORMATION:  
APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelle H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.

APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: HuIFN-alpha analog IFNa-N4  
US-08-954-395A-14

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKYSK 8  
Db 131 LTERKYSK 138

RESULT 21  
US-08-954-395A-15  
Sequence 15, Application US/08954395A  
Patent No. 6204022  
GENERAL INFORMATION:  
APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelle H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA

COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: HuIFN-alpha analog IFNa-N5  
US-08-954-395A-15

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
|||||||  
DB 131 LTERKXSP 138

RESULT 22  
US-08-954-395A-16  
Sequence 16, Application US/08954395A  
Patent No. 6204022  
GENERAL INFORMATION:  
APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelie H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
TITLE OF INVENTION: ANALOG  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A

FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: HuIFN-alpha analog IFNa-N6  
US-08-954-395A-16

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
|||||||  
DB 131 LTERKXSP 138

RESULT 23  
US-08-954-395A-17  
Sequence 17, Application US/08954395A  
Patent No. 6204022  
GENERAL INFORMATION:  
APPLICANT: Johnson, Howard M.  
APPLICANT: Subramaniam, Prem S.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Villarete, Lorelie H.  
APPLICANT: Campos, Jackeline  
APPLICANT: Chung, Albert D.  
APPLICANT: Li, Wayne W.  
APPLICANT: Liu, Philip T.  
TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
TITLE OF INVENTION: ANALOG  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates LLP  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/954,395A  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/631,328  
FILING DATE: 12-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J  
REGISTRATION NUMBER: 27008  
REFERENCE/DOCKET NUMBER: 5600-0001.35

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: HuIFN-alpha analog IFN-alpha-17  
US-08-954-395A-17

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LTERKXSP 8  
|||||||  
131 LTERKXSP 138

RESULT 24  
US-08-489-071A-16  
Sequence 16, Application US/08489071A  
Patent No. 6300474  
GENERAL INFORMATION:  
APPLICANT: PESTKA, SIDNEY  
TITLE OF INVENTION: SUPER PROTEINS INCLUDING INTERFERONS,  
TITLE OF INVENTION: INTERLEUKINS, ET AL.  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/489,071A  
FILING DATE: 09-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/257,784  
FILING DATE: 10-JUN-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/076,231  
FILING DATE: 11-JUN-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Fehner, Ph.D., Esq., Paul F.  
REGISTRATION NUMBER: 35,135  
REFERENCE/DOCKET NUMBER: 1705-1-002 CIPC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO

IMMEDIATE SOURCE:  
CLONE: Hu-IFN-alpha001  
US-08-489-071A-16

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LTERKXSP 8  
|||||||  
131 LTERKXSP 138

RESULT 25  
US-09-339-913B-75  
Sequence 75, Application US/09339913B  
Patent No. 6303344  
GENERAL INFORMATION:  
APPLICANT: Patten, Phillip  
APPLICANT: Stemmer, William P.C.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING  
FILE REFERENCE: 02-020503US  
CURRENT APPLICATION NUMBER: US/09/339,913B  
CURRENT FILING DATE: 1999-06-24  
PRIOR APPLICATION NUMBER: 08/769,062  
PRIOR FILING DATE: 1996-12-18  
PRIOR APPLICATION NUMBER: 08/198,431  
PRIOR FILING DATE: 1994-02-17  
PRIOR APPLICATION NUMBER: 08/425,684  
PRIOR FILING DATE: 1995-04-18  
PRIOR APPLICATION NUMBER: 08/537,874  
PRIOR FILING DATE: 1995-10-30  
NUMBER OF SEQ ID NOS: 101  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 75  
LENGTH: 166  
TYPE: PRT  
ORGANISM: consensus alpha interferon  
US-09-339-913B-75

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LTERKXSP 8  
|||||||  
131 LTERKXSP 138

Search completed: January 15, 2002, 08:40:28  
Job time: 295 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 15, 2002, 08:40:34 ; Search time 35.65 Seconds  
(without alignments)  
32.824 Million cell updates/sec

Title: US-09-424-080A-1  
Perfect score: 42  
Sequence: 1 LTRKXSP 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 50 summaries

Database :

1: SP:archaea:\*  
2: SP:bacteria:\*  
3: SP:fungi:\*  
4: SP:human:\*  
5: SP:invertebrate:\*  
6: SP:mammal:\*  
7: SP:mhc:\*  
8: SP:organelle:\*  
9: SP:phage:\*  
10: SP:plant:\*  
11: SP:rodent:\*  
12: SP:virus:\*  
13: SP:vertebrate:\*  
14: SP:unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	166	4 Q9UMJ3	Q9UMJ3 homo sapien
2	42	100.0	181	4 Q14608	Q14608 homo sapien
3	42	100.0	189	4 Q14605	Q14605 homo sapien
4	42	100.0	189	4 Q14639	Q14639 homo sapien
5	42	100.0	189	4 Q14607	Q14607 homo sapien
6	36	85.7	108	6 Q9N106	Q9N106 equus caball
7	36	85.7	170	6 Q29114	Q29114 sus scrofa
8	36	85.7	170	6 Q29115	Q29115 sus scrofa
9	36	85.7	730	10 Q9S9M5	Q9S9M5 arabidopsis
10	34	81.0	181	3 Q13619	Q13619 schizosacch
11	34	81.0	577	5 Q35995	Q35995 vaitimorpha
12	34	81.0	1154	5 Q9V6S9	Q9V6S9 drosophila
13	33	78.6	110	10 Q9SXY5	Q9SXY5 arabidopsis
14	33	78.6	334	2 Q9CKT2	Q9CKT2 pasteurilla
15	33	78.6	767	11 Q9WTU7	Q9WTU7 mus musculu
16	32	76.2	83	5 Q9V8W6	Q9V8W6 drosophila
17	32	76.2	400	5 Q9VBY9	Q9VBY9 drosophila
18	32	76.2	414	10 Q9SX74	Q9SX74 arabidopsis
19	32	76.2	573	5 Q23323	Q23323 caenorhabdi

20	32	76.2	1528	5 Q95022	Q95022 cryptospori
21	31	73.8	60	12 Q9IE09	Q9IE09 cotton leaf
22	31	73.8	113	2 Q9F554	Q9F554 escherichia
23	31	73.8	118	12 Q88551	Q88551 tomato yell
24	31	73.8	118	12 Q73583	Q73583 cotton leaf
25	31	73.8	118	12 Q90DF8	Q90DF8 tomato leaf
26	31	73.8	118	12 Q9IGY3	Q9IGY3 tobacco lea
27	31	73.8	118	12 Q9IGX7	Q9IGX7 tobacco gem
28	31	73.8	118	12 Q99DR5	Q99DR5 chili leaf
29	31	73.8	136	11 Q61717	Q61717 mus musculu
30	31	73.8	176	11 Q9D380	Q9D380 mus musculu
31	31	73.8	190	11 Q61716	Q61716 mus musculu
32	31	73.8	190	11 Q61718	Q61718 mus musculu
33	31	73.8	190	11 Q61719	Q61719 mus musculu
34	31	73.8	197	2 Q06983	Q06983 bacillus su
35	31	73.8	199	4 Q9Y6W8	Q9Y6W8 homo sapien
36	31	73.8	201	2 Q45137	Q45137 bacteroides
37	31	73.8	239	2 Q924D2	Q924D2 escherichia
38	31	73.8	261	2 P96679	P96679 bacillus su
39	31	73.8	275	2 P94124	P94124 acinetobact
40	31	73.8	285	3 Q00875	Q00875 fusarium so
41	31	73.8	322	4 Q92780	Q92780 homo sapien
42	31	73.8	401	1 Q59114	Q59114 pyrococcus
43	31	73.8	439	2 Q9RCV4	Q9RCV4 salmonella
44	31	73.8	510	2 Q9RK66	Q9RK66 streptomyce
45	31	73.8	589	2 Q9RMV4	Q9RMV4 bacillus an
46	31	73.8	603	2 Q9L217	Q9L217 streptomyce
47	31	73.8	727	3 Q9P6M8	Q9P6M8 schizosacch
48	31	73.8	804	3 Q00089	Q00089 aspergillus
49	31	73.8	804	3 Q93933	Q93933 aspergillus
50	31	73.8	893	2 Q9X1G2	Q9X1G2 thermotoga

## ALIGNMENTS

RESULT 1	
Q9UMJ3	PRELIMINARY; PRT; 166 AA.
AC Q9UMJ3;	
DT 01-MAY-2000 (TREMBLrel. 13, Created)	
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE IFNA PROTEIN (FRAGMENT).	
GN IFNA.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=8329241; PubMed=6310510;	
RA Weber H., Weissmann C.;	
RT "Formation of genes coding for hybrid proteins by recombination	
RT between related, cloned genes in E. coli."	
RL Nucleic Acids Res. 11:5661-5669(1983).	
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA	
CC FAMILY.	
EMBL; M29884; AAA52714.1; -.	
DR HSSP; P01563; ZHIE.	
DR Interpro; IPR000471; Interferon_abd.	
DR Pfam; PF00143; Interferon_1.	
DR PRINTS; PR00266; INTERFERONAB.	
DR Prodom; PD000550; Interferon_abd. 1.	
DR SMART; SM00076; IFabd. 1.	
DR PROSITE; PS00252; INTERFERON_A-B-D; 1.	
FT Antiviral; Cytokine.	
FT NON_TER 1	
SQ SEQUENCE 166 AA; 19386 MW; 4152EA2A78361BB8 CRC64;	
Query Match	100.0%; Score 42; DB 4; Length 166;
Best Local Similarity	100.0%; Pred. No. 0.65;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRKXSP 8  
 DB 131 LTRKXSP 138

RESULT 2  
 ID 014608 PRELIMINARY; PRT; 181 AA.  
 AC 014608;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE LEUCOCYTE INTERFERON-ALPHA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85056523; PubMed=6548765;  
 RA Gren E., Berzin V.M., Jansone I., Tsimanis A., Vishnevsky Y.,  
 RA Apsalons U.;  
 RT "Novel human leukocyte interferon subtype and structural comparison of  
 RT alpha interferon genes.";  
 RL J. Interferon Res. 4:609-617(1984).  
 CC -I- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
 CC EMBL; M28586; AAA36041.1; -.  
 DR HSSP; P01563; 2HE.  
 DR Interpro: IPR000471; Interferon\_abd.  
 DR Pfam: PF00143; Interferon\_1.  
 DR PRINTS: PR00266; INTERFERONAB.  
 DR Prodom: PD000550; Interferon\_abd; 1.  
 DR SMART; SM00076; IFabd; 1.  
 DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 DR Antiviral; Cytokine; Signal.  
 KM SEQUENCE 181 AA; 20878 MW; 3DB45120764EBABC CRC64;  
 SQ

Query Match 100.0%; Score 42; DB 4; Length 181;  
 Best Local Similarity 100.0%; Pred. No. 0.71;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRKXSP 8  
 DB 146 LTRKXSP 153

RESULT 3  
 ID 014605 PRELIMINARY; PRT; 189 AA.  
 AC 014605;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE INTERFERON-ALPHA 13 PRECURSOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RX Submitted (JAN-1994) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86037205; PubMed=4057246;  
 RA Hencho K., Brosius J., Fujisawa A., Fujisawa J.T., Haynes J.R.,  
 RA Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,  
 RA Toookero K., Waelchli M., Nagata S., Weissmann C.;  
 RT "Structural relationship of human interferon alpha genes and

RT pseudogenes.";  
 RL J. Mol. Biol. 185:227-260(1985).  
 CC -I- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
 CC EMBL; X75934; CAA53538.1; -.  
 DR EMBL; A07163; CAA00632.1; -.  
 DR HSSP; P01563; 2HE.  
 DR Interpro: IPR000471; Interferon\_abd.  
 DR Pfam: PF00143; Interferon\_1.  
 DR PRINTS: PR00266; INTERFERONAB.  
 DR Prodom: PD000550; Interferon\_abd; 1.  
 DR SMART; SM00076; IFabd; 1.  
 DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 KM Antiviral; Cytokine; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 189  
 FT SIGNAL 24 189  
 SQ SEQUENCE 189 AA; 21697 MW; 442F8B8754D88398 CRC64;

Query Match 100.0%; Score 42; DB 4; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.74;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRKXSP 8  
 DB 154 LTRKXSP 161

RESULT 4  
 ID 014639 PRELIMINARY; PRT; 189 AA.  
 AC 014639;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE LEUCOCYTE INTERFERON PRECURSOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87024453; PubMed=3767336;  
 RA Saveliev V.I., Zlochevsky M.L., Sorokin A.V., Naroditskaya V.A.,  
 RA Bolotin A.P., Demyanova N.G., Kozlov Y.I., Neznanov N.S.,  
 RA Gazaryan K.G., Monastyrskaya G.S., Sverdlov E.D.;  
 RT "[Cloning and the determination of the nucleotide sequences in 2 genes  
 RT of human leukocyte interferons].";  
 RL Antibiot. Med. Biotechnol. 31:592-596(1986).  
 CC -I- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
 CC EMBL; M38289; AAA59165.1; -.  
 DR HSSP; P01563; 2HE.  
 DR Interpro: IPR000471; Interferon\_abd.  
 DR Pfam: PF00143; Interferon\_1.  
 DR PRINTS: PR00266; INTERFERONAB.  
 DR Prodom: PD000550; Interferon\_abd; 1.  
 DR SMART; SM00076; IFabd; 1.  
 DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 KM Antiviral; Cytokine; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 189  
 FT SIGNAL 24 189  
 SQ SEQUENCE 189 AA; 21781 MW; 9DEB31870F1A88A1 CRC64;

Query Match 100.0%; Score 42; DB 4; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.74;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRKXSP 8  
 DB 154 LTRKXSP 161

```

RESULT 5
ID 014607 PRELIMINARY: PRT: 189 AA.
AC 014607:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE INTERFERON-ALPHA-J1 (IPN-ALPHA-J1).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86005847; PubMed=2995168;
RA Cohen S., Velan B., Grosfeld H., Shalita Z., Leitner M.,
RA Shalerman A.;
RT "Cloning, expression and biological activity of a new variant of human
interferon alpha identified in virus induced lymphoblastoid cells.";
Dev. Biol. 60:111-122(1985).
-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
CC EMBL; M34913; AAA36039.1; -.
DR HSSP; P01563; 2HE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; Ifabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
SQ SEQUENCE 189 AA; 22048 MW; 2AF6F48447BB72B3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 42; DB 4; Length 189;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKXSP 8
Db 154 LTERKXSP 161

RESULT 6
ID 09N106 PRELIMINARY: PRT: 108 AA.
AC 09N106:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE INTERFERON ALPHA-1 (FRAGMENT).
GN IFN1A.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20082971; PubMed=10613847;
RA Caetano A.R., Shine Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA Bowling A.T., Murray J.D.;
RT "A comparative gene map of the horse (Equus caballus).";
Genome Res. 9:1239-1246(1999).
-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
CC EMBL; AF135017; AAF29603.1; -.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; Ifabd; 1.

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DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 12420 MW; 028CA54FFA97FACD CRC64;

Query Match
Best Local Similarity 85.7%; Score 36; DB 6; Length 108;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKXSP 8
Db 95 LOEKXSP 102

RESULT 7
ID 029114 PRELIMINARY: PRT: 170 AA.
AC 029114:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE SHORT TYPE I INTERFERON PRECURSOR.
GN SPI IFN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-WHOLE CONCEPTUS (EMBRYO PLUS TROPHOBLAST);
RX MEDLINE=93374975; PubMed=7690039;
RA Lefevre F., Boulay V.;
RT "A novel and atypical type one interferon gene expressed by
trophoblast during early pregnancy.";
J. Biol. Chem. 268:19760-19768(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-WHOLE CONCEPTUS (EMBRYO PLUS TROPHOBLAST);
RX MEDLINE=86232600; PubMed=3714490;
RA von Heijne G.;
RT "A new method for predicting signal sequence cleavage sites.";
Nucleic Acids Res. 14:4683-4690(1986).
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
CC EMBL; Z22706; CAA80407.1; -.
DR HSSP; P01563; 1ITE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; Ifabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Signal.
FT SIGNAL 1
FT CHAIN 22 170 POTENTIAL.
FT VARIANT 88 88 S -> G.
FT VARIANT 101 101 N -> T.
SQ SEQUENCE 170 AA; 19906 MW; FED195EAFDD99AAB CRC64;

Query Match
Best Local Similarity 85.7%; Score 36; DB 6; Length 170;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKXSP 8
Db 146 LTERKXSP 153

RESULT 8
Q29115

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ID 029115 PRELIMINARY; PRT; 170 AA.
AC 029115;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE SHORT TYPE I INTERFERON PRECURSOR.
GN SPT IFN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LARGE WHITE BREED; TISSUE=LIVER;
RX MEDLINE=86232600; PubMed=3714490;
RA von Heijne G.;
RT "A new method for predicting signal sequence cleavage sites.";
RL Nucleic Acids Res. 14:4683-4690(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LARGE WHITE BREED; TISSUE=LIVER;
RX MEDLINE=87174805; PubMed=3550702;
RA Slinger D.S., Parent L.J., Ehrlich R.;
RT "Identification and DNA sequence of an interspersed repetitive DNA element in the genome of the miniature swine.";
RL Nucleic Acids Res. 15:2780-2780(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=LARGE WHITE BREED; TISSUE=LIVER;
RX MEDLINE=93374975; PubMed=7690039;
RA Lefevre F., Boulay V.;
RT "A novel and atypical type one interferon gene expressed by trophoblast during early pregnancy.";
RL J. Biol. Chem. 268:19760-19768(1993).
CC -I- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.
CC EMBL: Z22707; CAAB0408.1; -.
DR HSSP; P01563; IYF.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B-D; 1.
KW Antiviral; Cytokine; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 170 SHORT TYPE I INTERFERON.
FT SEQUENCE 170 AA; 19663 MW; 563F7D2AE716AF51 CRC64;

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Query Match 85.7%; Score 36; DB 6; Length 170;  
 Best Local Similarity 87.5%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 LTERKXSP 8
Db 146 LKERKXSP 153

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RESULT 9  
 Q9S9M5 PRELIMINARY; PRT; 730 AA.  
 AC Q9S9M5;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE T24D18.20 PROTEIN.  
 GN T24D18.20.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Liu S.X., Yu G., Sakano H., Jhaveri A., Lee J.M., Lenz C., Pham P.,
RA Tortum M., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
RA Howng B., Koo T., Li J., Liu A., Vayenberg M., Altafi H., Brooks S.,
RA Buehler E., Chao Q., Conn L., Conway A., Hansen N., Johnson-Hopson C.,
RA Khan S., Kim C., Lam C., Nguyen M., Palm C., Shinn P., Tambunga G.,
RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RT "The sequence of BAC T24D18 from Arabidopsis thaliana chromosome 1.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC EMBL: AC010924; AF18507.1; -.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actite.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00221; STYKC; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 730 AA; 81210 MW; B51DB48D95C73B5 CRC64;

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Query Match 85.7%; Score 36; DB 10; Length 730;  
 Best Local Similarity 75.0%; Pred. No. 45;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LTERKXSP 8
Db 224 LTRKXSP 231

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RESULT 10  
 O13619 PRELIMINARY; PRT; 181 AA.  
 AC O13619;  
 DT 01-JAN-1998 (TREMblrel. 05, Created)  
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
 DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE P1028 PROTEIN (HYPOTHETICAL 20.3 KDA PROTEIN).  
 GN P1028 OR SPB22H7.03.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 OX NCBI\_TaxID=4896;  
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972 H-;
 RA Kushida N., Yamazaki S., Tanaka T., Jinno K., Halkawa Y., Yamazaki J.,
 RA Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai M., Aoki K.,
 RA Ogura K., Otsuka R., Kudo Y., Yanagida M., Machida M., Zhang M.Q.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972H-;
 RA Murphy L., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB004535; BAA21407.1; -.
 DR EMBL; AL590883; CAC37371.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 181 AA; 20293 MW; 2D6A1B61F0FD51B8 CRC64;



Query Match  
Best Local Similarity 100.0%; Score 33; DB 10; Length 110;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 EKKYSP 8  
Db 36 EKKYSP 41

## RESULT 14

O9CKT2 PRELIMINARY; PRT; 334 AA.  
AC O9CKT2;  
DT 01-JUN-2001 (TREMblrel. 17, Created)  
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
GN HPA.  
OS HPA OR PM1524.  
SS Pasteurella multocida.  
CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Pasteurella.  
OX NCBI\_TaxID=747;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PM70;  
RX MEDLINE=21145866; PubMed=11248100;  
RA May B.J., Zhang O., Li L., Paustian M.L., Whittam T.S., Kapur V.;  
RT "Complete genomic sequence of Pasteurella multocida Pm70.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).  
CC -1- SIMILARITY: BELONGS TO THE ARAC/XLYS FAMILY OF TRANSCRIPTIONAL  
CC REGULATORS.  
DR EMBL: AE006189; AAK03608.1; -  
DR InterPro: IPR000005; HTHARAC.  
DR Pfam: PF00165; HTH\_ARAC.1.  
DR PRINTS: PR00032; HTHARAC.  
DR SMART: SM00342; HTH\_ARAC.1.  
DR PROSITE: PS00041; HTH\_ARAC\_FAMILY\_1; UNKNOWN\_1.  
DR PROSITE: PS01124; HTH\_ARAC\_FAMILY\_2; 1.  
KM Complete proteome: DNA-binding; Transcription regulation.  
SQ SEQUENCE 334 AA; 39714 MW; 8532929C52246503 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 33; DB 2; Length 334;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 EKKYSP 8  
Db 214 EKKYSP 219

## RESULT 15

O9WTU7 PRELIMINARY; PRT; 767 AA.  
AC O9WTU7;  
DT 01-NOV-1999 (TREMblrel. 12, Created)  
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
DE APOPTOSIS-LINKED PROTEIN 4, DELTAC FORM (FRAGMENT).  
GN POC11 OR ALG-4.  
OS Mus musculus (Mouse).  
SS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99244237; PubMed=10229231;  
RA Lacana E., D'Adamo L.;  
RT "Regulation of fas ligand expression and cell death by apoptosis-  
linked gene 4.";  
RL Nat. Med. 5:542-547(1999).  
DR EMBL: AF055668; AAD20941.1; -  
DR HSSP: P05055; ISRO.

DR MGD: MGI:1341788; Pdoc11.  
DR InterPro: IPR000110; Ribosomal\_S1.  
DR InterPro: IPR003029; S1.  
DR Pfam: PF00575; S1; 4.  
DR PRINTS: PR00681; RIBOSOMALS1.  
DR SMART: SM00316; S1; 6.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 767 AA; 84512 MW; 81B692B073E697FA CRC64;

Query Match  
Best Local Similarity 100.0%; Score 33; DB 11; Length 767;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 EKKYSP 8  
Db 101 EKKYSP 106

## RESULT 16

O9V8W6 PRELIMINARY; PRT; 83 AA.  
AC O9V8W6;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DE 01-MAY-2000 (TREMblrel. 13, Last annotation update)  
GN CG16926.  
OS Drosophila melanogaster (Fruit fly).  
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY.  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.E., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,  
RA Jaitani M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclab J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector A.C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*."  
 Science 287:2185-2195(2000).  
 DR EMBL; AE003795; AAF57541.1;  
 DR FlyBase; FBgn0040732; CG16926.  
 SQ SEQUENCE 83 AA; 9420 MW; 43A99D5F8BC2B680 CRC64;

Query Match 76.2%; Score 32; DB 5; Length 83;  
 Best Local Similarity 62.5%; Pred. No. 35;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTRKXSP 8  
 ||:||||  
 Db 44 LTRKXSP 51

RESULT 17  
 Q9VBY9 PRELIMINARY; PRT; 400 AA.  
 ID 09VBY9;  
 AC 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CG13649 PROTEIN.  
 GN CG13649.  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 ON NCBI\_Taxid=7227;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY.  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 Ananidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Miklos G.L.G.,  
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Pfiffner B.D.,  
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 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
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 Burks K.C., Bussan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,  
 Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegam C.,  
 Jaitani M., Kalush F., Karpen G.H., Ke Z., Kenton J.A., Ketchum K.A.,  
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 Nelson D.R., Nelson K.A., Nixon K., Pollard J., Puri V., Reese M.G.,  
 Palazzolo M., Pittman G.S., Pan S., Roldan C., Scheeler F., Shen H.,  
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 Spier E., Spidling A.C., Stapleton M., Strong R., Sun E.,  
 Svrtk R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,  
 Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Zheng H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*."  
 Science 287:2185-2195(2000).

DR EMBL; AE003750; AAF56387.1;  
 DR FlyBase; FBgn0039267; CG13649.  
 DR InterPro; IPR003889; FYRICH\_C.  
 DR InterPro; IPR003888; FYRICH\_N.  
 DR SMART; SM00542; FYRC; 1.  
 DR SMART; SM00541; FYRN; 1.  
 SQ SEQUENCE 400 AA; 45117 MW; 71CA68BD6B50E3F CRC64;

Query Match 76.2%; Score 32; DB 5; Length 400;  
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTKXSP 8  
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 Db 77 TTKXSP 83

RESULT 18  
 Q9SX74 PRELIMINARY; PRT; 414 AA.  
 ID 09SX74;  
 AC 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE F11A17.2 PROTEIN (TIN15.3).  
 GN F11A17.2.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;  
 OC Eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 ON NCBI\_Taxid=3702;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Vysotskaya V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,  
 Lee J.M., Li J., Li J., Gonzalez A., Liu A., Liu K., Vaysberg M.,  
 Sakano H., Chin C., Choi E., Chou J., Altati H., Araujo R.,  
 Brooks S., Buehler E., Chao Q., Conn L., Conway A.B., Dunn P.,  
 Hansen N., Hong B., Huizar L., Khan S., Kim C., Palm C., Rowley D.,  
 Shin P., Walker M., Davis R.W., Ecker J.R., Federspiel N.A.,  
 Theologis A.;  
 RT "thaliana chloroplast genome 1 BAC F11A17 sequence."  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RC SEQUENCE FROM N.A.  
 RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,  
 Shin P., Altati H., Bei Q., Chin C., Chou J., Choi E., Conn L.,  
 Conway A., Gonzalez A., Hansen N., Hong B., Koo T., Lam B., Lee J.,  
 Lenz C., Li J., Liu A., Liu K., Liu S., Mukharzky N., Nguyen M.,  
 Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,  
 Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,  
 Ecker J.R.;  
 RT "Genomic sequence for Arabidopsis thaliana BAC TIN15 from chromosome 1."  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RC SEQUENCE FROM N.A.  
 RA Ecker J.R.;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RC SEQUENCE FROM N.A.  
 RA Ecker J.R.;  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RC SEQUENCE FROM N.A.  
 RA Cheuk R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,  
 Khan S., Kim C., Altati H., Bei B., Chin C., Chou J., Choi E.,  
 Conn L., Conway A., Gonzalez A., Hansen N., Hong B., Koo T., Lam B.,  
 Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharzky N.,  
 Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
 Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,  
 Theologis A., Ecker J.R.

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC007932; AAD49754.2; -  
 DR EMBL: AC020889; AAF79717.1; -  
 DR InterPro: IPR001926; PALP.  
 SO SEQUENCE 414 AA; 45332 MW; 2793ED561D95DD5 CRC64;

Query Match 76.2%; Score 32; DB 10; Length 414;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTERKYP 8  
 DB 32 LTERKYP 39

RESULT 19  
 Q23323 PRELIMINARY; PRT; 573 AA.

Q23323;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE ZC443.5 PROTEIN.  
 GN ZC443.5.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OC NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Baynes C.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Ritken L., Roopra A., Saunders D., Showkeen R.,  
 RA Smaison N., Smith A., Sonhammer E., Staden R., Sulston J.,  
 RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Woldman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 elegans."  
 RL Nature 368:32-38(1994).  
 DR EMBL: Z75553; CAA99950.1;  
 DR InterPro: IPR002213; UDPGT.  
 DR Pfam: PF00201; UDPGT.1.  
 SO SEQUENCE 573 AA; 65645 MW; 5429DJ3388BCB40F CRC64;

Query Match 76.2%; Score 32; DB 5; Length 573;  
 Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKYP 7  
 DB 475 LTERKYP 481

RESULT 20

ID 095022 PRELIMINARY; PRT; 1528 AA.

AC 095022;  
 DT 01-FEB-1997 (TREMblrel. 02, Created)  
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE P-ATPASE.  
 GN CPAA-El.

OS Cryptosporidium parvum.  
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
 OC Cryptosporidiidae; Cryptosporidium.  
 OC NCBI\_TaxID=5807;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KSU-1.  
 RA Zhu G., Kirumsov N., Upton S.J., Keithly J.S.;  
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U65981; AAC47833.1; -  
 DR HSSP: P04191; IEUL.  
 DR InterPro: IPR001757; E1-E2\_ATPase.  
 DR InterPro: IPR001454; Hydrolase.  
 DR Pfam: PF00122; E1-E2\_ATPase; 1.  
 DR Pfam: PF00702; Hydrolase; 1.  
 DR PRINTS: PR00119; CATAPASE.  
 DR PROSITE: PS00154; ATPASE\_E1\_E2; UNKNOWN\_1.  
 KW Hydrolase.

SO SEQUENCE 1528 AA; 168873 MW; 82AECB973C207D8B CRC64;

Query Match 76.2%; Score 32; DB 5; Length 1528;  
 Best Local Similarity 75.0%; Pred. No. 5.9e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LTERKYP 8  
 DB 242 LTERKYP 249

RESULT 21

ID 091E09 PRELIMINARY; PRT; 60 AA.

AC 091E09;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE AV2 PROTEIN (FRAGMENT).  
 GN AV2.  
 OS cotton leaf curl virus.  
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
 OC NCBI\_TaxID=53010;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B27-IR.  
 RX MEDLINE=20318672; PubMed=10859391;  
 RA Sanz A.T., Fralle A., Garcia-Arenal F., Zhou X., Robinson D.J.,  
 RA Khalid S., Butt T., Harrison B.D.;  
 RT "Multiple infection, recombination and genome relationships among  
 RT begomovirus isolates found in cotton and other plants in Pakistan."  
 RL J. Gen. Virol. 81:1839-1849(2000).  
 DR EMBL: AJ270861; CAB97098.1;  
 DR InterPro: IPR002511; GeminV\_VI.  
 DR Pfam: PF01524; GeminV\_VI; 1.  
 DR ProDom: PD002978; GeminV\_VI; 1.  
 FT NON\_TER  
 SO SEQUENCE 60 AA; 7035 MW; 113D7E8980D7EFBC CRC64;

Query Match 73.8%; Score 31; DB 12; Length 60;  
 Best Local Similarity 75.0%; Pred. No. 41;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LTERKYP 8  
 DB 27 LTERKYP 34

RESULT 22

ID 09F554 PRELIMINARY; PRT; 113 AA.

AC 09F554;  
 DT 01-MAR-2001 (TREMblrel. 16, Created)



DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
 DE RELAXOSOME COMPONENT.  
 GN NKA.  
 OS Escherichia coli.  
 OC Plasmid R721.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia  
 OC NCBI\_TaxID=562;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12; TRANSPOSON-TN7;  
 RA Samped G., Motomura K., Masuda S., Yamaguchi T., Ando K., Oishi T.,  
 RA Furuya N., Komano T., Mizobuchi K.;  
 RT "Organization and diversification of plasmid genomes: complete  
 RT nucleotide sequence of the R721 genome."  
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12; TRANSPOSON-TN7;  
 RC MEDLINE-93015772; PubMed-1400257;  
 RC Kim S., Komano T.;  
 RC "Nucleotide sequence of the R721 shuffleon."  
 RC J. Bacteriol. 174:7053-7058(1992).  
 DR EMBL: AP002527; BAB12623.1;  
 DR InterPro: IPR002145; CopeG\_HTH\_4.  
 DR Pfam: PF01402; HTH\_4; 1.  
 DR Plasmid.  
 KW SEQUENCE 113 AA; 13147 MW; C7D3B2406A25DA9C CRC64;  
 SQ

Query Match 73.8%; Score 31; DB 2; Length 113;  
 Best Local Similarity 62.5%; Pred. No. 76;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
 |||:|:|  
 Db 15 LTEREYAP 22

RESULT 23  
 088551  
 AC 088551; PRELIMINARY; PRT; 118 AA.  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
 DE PRECOAT PROTEIN.  
 GN V2.  
 OS Tomato yellow leaf curl virus (TYLCV).  
 OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
 OC NCBI\_TaxID=10832;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BANGALORE II, INDIA;  
 RA Chatchawankarnpanich O., Chiang B.T., Green S.K., Singh S.J.,  
 RA Melita P., Maxwell D.P.;  
 RT Submitted (Oct-1995) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U38239; AAB08928.1;  
 DR InterPro: IPR002511; Geminl\_VL.  
 DR Pfam: PF01524; Geminl\_VL; 1.  
 DR ProDom: PD002978; Geminl\_VL; 1.  
 KW Coat protein.  
 SQ SEQUENCE 118 AA; 13724 MW; 89E41A39BF7FF6B3 CRC64;

Query Match 73.8%; Score 31; DB 12; Length 118;  
 Best Local Similarity 75.0%; Pred. No. 79;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
 |||:|:|  
 Db 27 LVEKTYSP 34

RESULT 24  
 073583  
 AC 073583; PRELIMINARY; PRT; 118 AA.  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
 DE AV2 PROTEIN.  
 GN AV2.  
 OS cotton leaf curl virus.  
 OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
 OC NCBI\_TaxID=53010;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PAKISTAN;  
 RX MEDLINE-98227943; PubMed-9568988;  
 RA Zhou X., Liu Y., Robinson D.J., Harrison B.D.;  
 RT "Four DNA-A variants among Pakistani isolates of cotton leaf curl  
 RT virus and their affinities to DNA-A of geminivirus isolates from  
 RT okra."  
 RL J. Gen. Virol. 79:915-923(1998).  
 DR EMBL: A002449; CA05432.1;  
 DR EMBL: A002448; CA05426.1;  
 DR InterPro: IPR002511; Geminl\_VL.  
 DR Pfam: PF01524; Geminl\_VL; 1.  
 DR ProDom: PD002978; Geminl\_VL; 1.  
 SQ SEQUENCE 118 AA; 13721 MW; 72948EF3538BA408 CRC64;

Query Match 73.8%; Score 31; DB 12; Length 118;  
 Best Local Similarity 75.0%; Pred. No. 79;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
 |||:|:|  
 Db 27 LVEKTYSP 34

RESULT 25  
 090DE8  
 AC 090DE8; PRELIMINARY; PRT; 118 AA.  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
 DE PRE-COAT PROTEIN.  
 GN V2.  
 OS tomato leaf curl geminivirus.  
 OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
 OC NCBI\_TaxID=28350;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-TLCV-BD2;  
 RA Shih S.L., Tsai W.S., Nakha M.K., Maxwell D.P., Rashid M.H.,  
 RA Green S.K.;  
 RT "Molecular comparison of two tomato leaf curl viruses from  
 RT Bangladesh."  
 RL Zhifu Baohuixue Hui Huikan 40:436-437(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-TLCV-BD2;  
 RA Tsai W.S., Nakha M.K., Maxwell D.P., Rashid M.H., Green S.K.;  
 RT Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF168481; AAF04835.1;  
 DR InterPro: IPR002511; Geminl\_VL.  
 DR Pfam: PF01524; Geminl\_VL; 1.  
 DR ProDom: PD002978; Geminl\_VL; 1.  
 KW Coat protein.  
 SQ SEQUENCE 118 AA; 13704 MW; FD978795A13FE443 CRC64;

Query Match 73.8%; Score 31; DB 12; Length 118;  
Best Local Similarity 75.0%; Pred. No. 79;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 LTKKSP 8  
| | | | |  
Db 27 LTKKSP 34

Search completed: January 15, 2002, 08:45:34  
Job time: 300 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 15, 2002, 08:40:04 ; Search time 12.84 Seconds  
(without alignments)  
22.844 Million cell updates/sec

Title: US-09-424-080A-1

Perfect score: 42  
Sequence: 1 LTERKXSP 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	189	1	INA1_HUMAN
2	42	100.0	189	1	INA4_HUMAN
3	42	100.0	189	1	INA5_HUMAN
4	42	100.0	189	1	INA6_HUMAN
5	42	100.0	189	1	INA7_HUMAN
6	42	100.0	189	1	INA8_HUMAN
7	36	85.7	184	1	INA1_HORSE
8	36	85.7	184	1	INA2_HORSE
9	36	85.7	184	1	INA3_HORSE
10	36	85.7	184	1	INA4_HORSE
11	36	85.7	188	1	INA2_HUMAN
12	36	85.7	189	1	INA7_HUMAN
13	36	85.7	189	1	INA7_HUMAN
14	36	85.7	194	1	INA_FELCA
15	35	83.3	189	1	INA8_HUMAN
16	35	83.3	195	1	INO1_HORSE
17	34	81.0	528	1	LADI_MOUSE
18	33	78.6	189	1	INA4_HUMAN
19	32	76.2	114	1	FVE_FLAIVE
20	31	73.8	189	1	INA1_MOUSE
21	31	73.8	189	1	INA1_PIG
22	31	73.8	189	1	INA5_MOUSE
23	31	73.8	189	1	INA6_MOUSE
24	31	73.8	189	1	INA8_MOUSE
25	31	73.8	190	1	INA2_MOUSE
26	31	73.8	190	1	INA7_MOUSE
27	31	73.8	190	1	INA9_MOUSE
28	31	73.8	275	1	BLO3_PSEAE
29	31	73.8	545	1	FLIF_BUCAL
30	31	73.8	779	1	ZW10_HUMAN
31	31	73.8	959	1	NI00_YEAST
32	30	71.4	229	1	CSE4_YEAST
33	30	71.4	270	1	TPIS_CHILMU

## ALIGNMENTS

RESULT	1	STANDARD	PRT	189	AA
INA1_HUMAN					
ID	INA1_HUMAN				
AC	P01562				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	20-AUG-2001 (Rel. 40, Last annotation update)				
DE	INTERFERON ALPHA-1/13 PRECURSOR (INTERFERON ALPHA-D) (IEIF D).				
GN	IFNA1 AND IFNA13.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=81005094; PubMed=6157600;				
RA	Mantel N., Schwarstein M., Streull M., Panem S., Nagata S.,				
RA	Weissmann C.;				
RT	"The nucleotide sequence of a cloned human leukocyte interferon				
RL	cDNA.";				
RL	Gene 10:1-10(1980).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=80254543; PubMed=6157095;				
RA	Taniguchi T., Mantel N., Schwarstein M., Nagata S., Muramatsu M.,				
RA	Weissmann C.;				
RT	"Human leukocyte and fibroblast interferons are structurally				
RL	related.";				
RL	Nature 285:547-549(1980).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=81148795; PubMed=6163083;				
RA	Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,				
RA	McGardis R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;				
RT	"The structure of eight distinct cloned human leukocyte interferon				
RL	cDNAs.";				
RL	Nature 290:20-26(1981).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=85003592; PubMed=6479148;				
RA	Todoroko K., Kiousis D., Weissmann C.;				
RT	"Two non-allelic human interferon alpha genes with identical coding				
RL	regions.";				
RL	EMBO J. 3:1809-1812(1984).				
CC	-1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL				
CC	ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:				
CC	A PROTEIN KINASE AND AN OLIGADENYLATE SYNTHETASE.				
CC	-1- MISCELLANEOUS: INTERFERONS ALPHA-1 AND ALPHA-13 HAVE IDENTICAL				
CC	PROTEIN SEQUENCES.				
CC	-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA				
CC	FAMILY.				

057550 methanococ  
Q07788 saccharomyc  
P52891 saccharomyc  
P03160 woodchuck h  
P06275 woodchuck h  
P12898 woodchuck h  
P17396 woodchuck h  
P15402 white clove  
P78013 mycoplasma  
P05015 homo sapien  
P05002 homo sapien  
P05002 equus cabal  
Q95187 giraffa cam  
P54765 lotus japon  
P46072 vibrio fisc  
P38548 vicia faba

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DR  EMBL: J00210; AAB59403.1; -
DR  EMBL: V00537; CAA23798.1; -
DR  EMBL: V00538; CAA23799.1; -
DR  EMBL: X00803; CAA23581.1; -
DR  PIR: A01826; IYHVA1.
DR  PIR: C23285; C23285.
DR  HSSP: P01563; 2HTE.
DR  MIM: 147578; -
DR  MIM: 147660; -
DR  InterPro: IPR000471; Interferon_abd.
DR  Pfam: PF00143; Interferon; 1.
DR  PRINTS: PR00266; INTERFERONAB.
DR  ProDom: PD000550; Interferon_abd; 1.
DR  SMART: SM00076; IFab; 1.
DR  PROSITE: PS00252; INTERFERON_A_B_D; 1.
DR  CytoKine; Antiviral; Multigene family; Signal.
DR  SIGNAL 1 23
FT CHAIN 24 189 INTERFERON ALPHA-1/13.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
FT CONFLICT 137 137 A -> V (IN REF. 3).
SQ SEQUENCE 189 AA; 21725 MW; F32F9CB96960B69 CRC64;

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Query Match          100.0%; Score 42; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LTERKRYSP 8
Db 154 LTERKRYSP 161

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RESULT 2
ID INAA_HUMAN STANDARD; PRT; 189 AA.
AC P05014; P13358;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERFERON ALPHA-4 PRECURSOR (INTERFERON ALPHA-4B) (INTERFERON
DE ALPHA-M1) (INTERFERON ALPHA-76).
GN IFNA4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86037205; PubMed=4057246;
RA Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,
RA Hochstadt J., Kovacic T., Pasek M., Schambeck A., Schmid J.,
RA Todokoro K., Waelchli M., Nagata S., Weissmann C.;
RT "Structural relationship of human interferon alpha genes and
RT pseudogenes.";
RL J. Mol. Biol. 185:227-260(1985).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84307815; PubMed=6089830;
RA Lunane A.W., Belharz M.W., McMullen G.L., Macreadie I.G.,
RA Murphy M., Nisbet I.T., Novitski C.E., Woodrow G.C.;
RT "Nucleotide sequence and expression in E. coli of a human interferon-
RT alpha gene selected from a genomic library using synthetic
RT oligonucleotides.";

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RL Biochem. Int. 8:725-732(1984).
CC -I- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENTERYL SYNTHETASE.
CC -I- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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-----
DR  EMBL: X02955; CAA26701.1; -
DR  EMBL: M27318; AAB52726.1; -
DR  PIR: E23753; IYH04B.
DR  HSSP: P01563; 1ITF.
DR  MIM: 147564; -
DR  InterPro: IPR000471; Interferon_abd.
DR  Pfam: PF00143; Interferon; 1.
DR  PRINTS: PR00266; INTERFERONAB.
DR  ProDom: PD000550; Interferon_abd; 1.
DR  SMART: SM00076; IFab; 1.
DR  PROSITE: PS00252; INTERFERON_A_B_D; 1.
DR  CytoKine; Antiviral; Multigene family; Signal.
DR  SIGNAL 1 23
FT CHAIN 24 189 INTERFERON ALPHA-4.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
FT CONFLICT 74 74 T -> A (IN REF. 2).
FT CONFLICT 137 137 V -> E (IN REF. 2).
SQ SEQUENCE 189 AA; 21808 MW; 4198F9CC8E2A80C CRC64;

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Query Match          100.0%; Score 42; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LTERKRYSP 8
Db 154 LTERKRYSP 161

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RESULT 3
ID INA5_HUMAN STANDARD; PRT; 189 AA.
AC P01569;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERFERON ALPHA-5 PRECURSOR (INTERFERON ALPHA-G) (LEIF G) (INTERFERON
DE ALPHA-61).
GN IFNA5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86037205; PubMed=4057246;
RA Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,
RA Hochstadt J., Kovacic T., Pasek M., Schambeck A., Schmid J.,
RA Todokoro K., Waelchli M., Nagata S., Weissmann C.;
RT "Structural relationship of human interferon alpha genes and
RT pseudogenes.";
RL J. Mol. Biol. 185:227-260(1985).
[2]
RP SEQUENCE OF 57-189 FROM N.A.
RX TISSUE-Spleen;
RX MEDLINE=81148795; PubMed=6163083;
RA Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,

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RA McCondliss R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
RT "The structure of eight distinct cloned human leukocyte Interferon
RL cDNAs."
CC Nature 290:20-26(1981).
CC -I- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC -I- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X02956; CAA26702.1; -.
CC EMBL: V00541; CAA23802.1; -.
CC PIR: A01833; IYH0A7.
CC HSP: P01563; 2HIE.
CC MIM: 147565; -.
CC InterPro: IPR000471; Interferon_abd.
CC Pfam: PF00143; Interferon_1.
CC PRINTS: PR00266; INTERFERONAB.
CC PRODOM: PD000550; Interferon_abd; 1.
CC SMART: SM00076; IFab; 1.
CC PROSITE: PS00252; INTERFERON_A-B-D; 1.
CC DR Cytokine; Antiviral; Multigene family; Signal.
CC KW SIGNAL
CC FT CHAIN
CC FT DISULFID 24 189 INTERFERON ALPHA-5.
CC FT DISULFID 52 162 BY SIMILARITY.
CC FT DISULFID 52 162 BY SIMILARITY.
CC S0 SEQUENCE 189 AA; 21942 MW; C605992FE2E78043 CRC64;

Query Match 100.0%; Score 42; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKXSP 8
DB 154 LTERKXSP 161

RESULT 4
INAG_HUMAN STANDARD; PRT; 189 AA.
P05013;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERFERON ALPHA-6 PRECURSOR (INTERFERON ALPHA-K) (LEIF K) (INTERFERON
DE ALPHA-54).
DE IFNA6.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86037205; PubMed=4057246;
RA Henco K., Brosius J., Fujisawa J.-I., Haynes J.R.,
RA Hochstadt J., Kovacic T., Pasak M., Schambeck A., Schmid J.,
RA Toookoro K., Maechli M., Nagata S., Weissmann C.;
RA "Structural relationship of human Interferon alpha genes and
RA pseudogenes."
RT J. Mol. Biol. 185:227-260(1985).
CC -I- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC -I- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X02958; CAA26704.1; -.
CC PIR: A23753; IYH0I6.
CC HSP: P01563; 1IIF.
CC MIM: 147566; -.
CC InterPro: IPR000471; Interferon_abd.
CC Pfam: PF00143; Interferon_1.
CC PRINTS: PR00266; INTERFERONAB.
CC PRODOM: PD000550; Interferon_abd; 1.
CC DR SMART; SM00076; IFab; 1.
CC DR PROSITE; PS00252; INTERFERON_A-B-D; 1.
CC KW Cytokine; Antiviral; Multigene family; Signal.
CC FT CHAIN
CC FT DISULFID 24 189 INTERFERON ALPHA-6.
CC FT DISULFID 52 162 BY SIMILARITY.
CC S0 SEQUENCE 189 AA; 22140 MW; 8C7F3F90F12C562E CRC64;

Query Match 100.0%; Score 42; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKXSP 8
DB 154 LTERKXSP 161

RESULT 5
INAG_HUMAN STANDARD; PRT; 189 AA.
AC P01571;
21-JUL-1986 (Rel. 01, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERFERON ALPHA-17 PRECURSOR (INTERFERON ALPHA-I') (INTERFERON
DE ALPHA-T) (INTERFERON ALPHA-88).
DE IFNA17.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81201124; PubMed=6165082;
RA Lavin R.M., Adelman J., Dull T.J., Gross M., Goeddel D.V., Ullrich A.;
RA "DNA sequence of two closely linked human leukocyte Interferon
RA genes."
RT Science 212:1159-1162(1981).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85229953; PubMed=3891272;
RA Mizoguchi J., Pitha P.M., Raj N.B.K.;
RA "Efficient expression in Escherichia coli of two species of human
RA Interferon-alpha and their hybrid molecules."
RN DNA 4:221-232(1985).
RN [3]
RP SEQUENCE OF 14-189 FROM N.A.
RX MEDLINE=85235859; PubMed=4008999;
RA Lund B., von Gabain A., Edlund T., Ny T., Lundgren E.;
RA "Differential expression of interferon genes in a substrain of
RA Namalwa cells."
RT J. Interferon Res. 5:229-238(1985).
CC -I- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL

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CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
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 CC -----  
 CC DR EMBL: M1026; AAA52725.1; -  
 CC DR EMBL: V00532; CAA23793.1; -  
 CC DR EMBL: M71246; AAA52713.1; -  
 CC DR PIR: A01835; IVHUA9.  
 CC DR PIR: A22255; A22255.  
 CC DR HSSP: P01563; 1ITE.  
 CC DR MIM: 147583; -  
 CC DR InterPro: IPR000471; Interferon\_abd.  
 CC DR Pfam: PF00143; Interferon; 1.  
 CC DR PRINTS: PR00266; INTERFERONAB.  
 CC DR ProDom: PD000550; Interferon\_abd; 1.  
 CC DR SMART: SM00076; Ifabd; 1.  
 CC DR PROSITE: PS00252; INTERFERON\_A\_B\_D; 1.  
 CC DR CYTOKINE; Antiviral; Multigene family; Signal.  
 CC KW SIGNAL 1 189 INTERFERON ALPHA-17.  
 CC FT CHAIN 24 189 BY SIMILARITY.  
 CC FT DISULFID 24 122 BY SIMILARITY.  
 CC FT DISULFID 52 162 H -> P (IN REF. 1).  
 CC FT CONFLICT 57 57 I -> R (IN REF. 3).  
 CC FT CONFLICT 184 184  
 CC SQ SEQUENCE 189 AA; 21728 MW; 0448EAEAB9D7FC32 CRC64;

Query Match 100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKYPSP 8  
 DB 154 LTERKYPSP 161

RESULT 6  
 INAK\_HUMAN STANDARD; PRT; 189 AA.  
 AC P01568;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE INTERFERON ALPHA-21 PRECURSOR (INTERFERON ALPHA-F) (LEIF F).  
 GN IFNA21.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81148795; PubMed=6163083;  
 RA Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,  
 RA McCandliss R., Seeburg P.H., Ullrich A., Vetterton E., Gray P.W.;  
 RT "The structure of eight distinct cloned human leukocyte interferon  
 RT cDNAs.";  
 RL Nature 290:20-26(1981).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RN Gren E.Y., Berzin V.M., Tsimanis A.Y., Apsalon U.R., Vishnevskii Y.I.,  
 RA Yansore I.V., Dishler A.V., Pudova N.V., Smorodinsev A.A.,  
 RA Iovlev V.I., Stepanov A.N., Feldmane G.Y., Meldrats Y.A., Lozha V.P.,  
 RA Kavshan V.M., Efimov V.A., Sverdlov E.D.;  
 RT "A new type of leukocytic interferon.";

RL DOK1. Biochem. 269:91-95(1983).  
 CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
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 CC -----  
 CC DR EMBL: M12350; AAA52718.1; -  
 CC DR EMBL: V00340; CAA23801.1; -  
 CC DR EMBL: X00145; CAA24980.1; -  
 CC DR PIR: A01832; IVHUF.  
 CC DR HSSP: P01563; 2HIE.  
 CC DR MIM: 147584; -  
 CC DR InterPro: IPR000471; Interferon\_abd.  
 CC DR Pfam: PF00143; Interferon; 1.  
 CC DR PRINTS: PR00266; INTERFERONAB.  
 CC DR ProDom: PD000550; Interferon\_abd; 1.  
 CC DR SMART: SM00076; Ifabd; 1.  
 CC DR PROSITE: PS00252; INTERFERON\_A\_B\_D; 1.  
 CC DR CYTOKINE; Antiviral; Multigene family; Signal.  
 CC KW SIGNAL 1 189 INTERFERON ALPHA-21.  
 CC FT CHAIN 24 189 BY SIMILARITY.  
 CC FT DISULFID 24 122 BY SIMILARITY.  
 CC FT DISULFID 52 162 M -> L (IN REF. 2).  
 CC FT CONFLICT 119 119  
 CC SQ SEQUENCE 189 AA; 21759 MW; 05B78D86929059B3 CRC64;

Query Match 100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKYPSP 8  
 DB 154 LTERKYPSP 161

RESULT 7  
 INAL\_HORSE STANDARD; PRT; 184 AA.  
 AC P05003;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 01-MAR-1989 (Rel. 10, Last annotation update)  
 DE INTERFERON ALPHA-1 PRECURSOR.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87053170; PubMed=3022999;  
 RA Himmler A., Hauptmann R., Adolf G.R., Swetly P.;  
 RT "Molecular cloning and expression in Escherichia coli of equine type  
 RT I interferons.";  
 RL DNA 5:345-356(1986).  
 RL [2]  
 RP FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
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EMBL: M14540; AAA30953.1; -

DR PIR: A24912; IYHOA1.

DR HSSP: P01563; 2HIE.

DR InterPro: IPR000471; Interferon\_abd.

DR Pfam: PF00143; Interferon\_1.

DR PRINTS: PR00286; INTERFERONAB.

DR PRODOM: PD000550; Interferon\_abd; 1.

DR SMART: SM00076; IFabd; 1.

DR PROSITE: PS00252; INTERFERON\_A-B-D; 1.

KW Cytokine; Antiviral; Multigene family; Signal.

KW SIGNAL

FT CHAIN 1 23 INTERFERON ALPHA-1.

FT DISULFID 24 122 BY SIMILARITY.

FT DISULFID 52 162 BY SIMILARITY.

SC SEQUENCE 184 AA; 20808 MW; 9E860B8CD05C83E6 CRC64;

Query Match

Best Local Similarity 85.7%; Score 36; DB 1; Length 184;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTERKXSP 8

Db 154 LOEKXSP 161

RESULT 8

INAA3\_HORSE STANDARD; PRT; 184 AA.

AC P05004;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 01-MAR-1989 (Rel. 10, Last annotation update)

DE INTERFERON ALPHA-2 PRECURSOR.

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI\_TaxID=9796;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=87053170; PubMed=3022999;

RA Himmler A., Hauptmann R., Adolf G.R., Swelly P.;

RT "Molecular cloning and expression in Escherichia coli of equine type I interferons.";

RT DNA 5:345-356(1986).

CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES: A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.

CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.

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CC -----

EMBL: M14541; AAA30950.1; -

DR EMBL: A15987; CAA01258.1; -

DR PIR: B24912; IYHOA2.

DR HSSP: P01563; 2HIE.

DR InterPro: IPR000471; Interferon\_abd.

DR Pfam: PF00143; Interferon\_1.

DR PRINTS: PR00266; INTERFERONAB.

DR PRODOM: PD000550; Interferon\_abd; 1.

DR SMART: SM00076; IFabd; 1.

DR PROSITE: PS00252; INTERFERON\_A-B-D; 1.

KW Cytokine; Antiviral; Multigene family; Signal.

KW SIGNAL

FT CHAIN 1 23 INTERFERON ALPHA-1.

FT DISULFID 24 122 BY SIMILARITY.

FT DISULFID 52 162 BY SIMILARITY.

SC SEQUENCE 184 AA; 20782 MW; 4C15D991ECA6D24A CRC64;

Query Match

Best Local Similarity 85.7%; Score 36; DB 1; Length 184;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DR PROSITE: PS00252; INTERFERON\_A-B-D; 1.

KW Cytokine; Antiviral; Multigene family; Signal.

KW SIGNAL

FT CHAIN 1 23 INTERFERON ALPHA-2.

FT DISULFID 24 122 BY SIMILARITY.

FT DISULFID 52 162 BY SIMILARITY.

SC SEQUENCE 184 AA; 20877 MW; FC15DC7D811C68EC CRC64;

Query Match

Best Local Similarity 85.7%; Score 36; DB 1; Length 184;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTERKXSP 8

Db 154 LOEKXSP 161

RESULT 9

INAA3\_HORSE STANDARD; PRT; 184 AA.

AC P05005;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 01-MAR-1989 (Rel. 10, Last annotation update)

DE INTERFERON ALPHA-3 PRECURSOR.

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI\_TaxID=9796;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=87053170; PubMed=3022999;

RA Himmler A., Hauptmann R., Adolf G.R., Swelly P.;

RT "Molecular cloning and expression in Escherichia coli of equine type I interferons.";

RT DNA 5:345-356(1986).

CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES: A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.

CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.

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CC -----

EMBL: M14542; AAA30951.1; -

DR EMBL: A16555; CAA01292.1; -

DR PIR: C24912; IYHOA3.

DR HSSP: P01563; 2HIE.

DR InterPro: IPR000471; Interferon\_abd.

DR Pfam: PF00143; Interferon\_1.

DR PRINTS: PR00266; INTERFERONAB.

DR PRODOM: PD000550; Interferon\_abd; 1.

DR SMART: SM00076; IFabd; 1.

DR PROSITE: PS00252; INTERFERON\_A-B-D; 1.

KW Cytokine; Antiviral; Multigene family; Signal.

KW SIGNAL

FT CHAIN 1 23 INTERFERON ALPHA-3.

FT DISULFID 24 122 BY SIMILARITY.

FT DISULFID 52 162 BY SIMILARITY.

SC SEQUENCE 184 AA; 20782 MW; 4C15D991ECA6D24A CRC64;

Query Match

Best Local Similarity 85.7%; Score 36; DB 1; Length 184;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY      1 LTERKYS 8
DB      154 LOEKKYS 161

RESULT 10
ID      INA4_HORSE STANDARD; PRT; 184 AA.
AC      P05006;
DT      13-AUG-1987 (Rel. 05, Created)
DT      13-AUG-1987 (Rel. 05, Last sequence update)
DT      01-MAR-1989 (Rel. 10, Last annotation update)
DE      INTERFERON ALPHA-4 PRECURSOR.
OS      Equus caballus (Horse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID:9796;
RN      [1]
RP      SEQUENCE FROM N.A.
RT      MEDLINE=87053170; PubMed=3022999;
RA      Hammler A., Hauptmann R., Adolf G.R., Swelly P.;
RT      "Molecular cloning and expression in Escherichia coli of equine type
RT      I interferons".
RL      DNA 5.345-356(1986).
CC      -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC      ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC      A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC      -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC      FAMILY.
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CC      -----
DR      EMBL: M14543; AAA30952.1; -.
DR      PIR: D24912; IVHOA4.
DR      HSSP: P01563; IYF.
DR      InterPro: IPR000471; Interferon_abd.
DR      Pfam: PF00143; Interferon_1.
DR      PRINTS: PR00266; INTERFERONAB.
DR      ProDom: PD000550; Interferon_abd; 1.
DR      SMART: SM00076; IFabd; 1.
DR      PROSITE: PS00252; INTERFERON_A_B_D; 1.
DR      Cytokine; Antiviral; Multigene family; Signal.
DR      SIGNAL
FT      CHAIN 1 24 184 INTERFERON ALPHA-4.
FT      DISULFID 24 122 BY SIMILARITY.
FT      DISULFID 52 162 BY SIMILARITY.
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Query Match 85.7%; Score 36; DB 1; Length 184;
Best Local Similarity 87.5%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 LTERKYS 8
DB      154 LOEKKYS 161

RESULT 11
ID      INA2_HUMAN STANDARD; PRT; 188 AA.
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DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      20-AUG-2001 (Rel. 40, Last annotation update)
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RP      SEQUENCE FROM N.A.
RT      MEDLINE=81052322; PubMed=6159538;
RA      Goeddel D.V., Yelveton E., Ullrich A., Heyneker H.L., Mizzari G.,
RT      Holmes W., Seeburg P.H., Dull T.J., May L., Stebbins N., Crea R.,
RT      Maeda S., McCandless R., Sloma A., Tabor J.M., Gross M.,
RT      Familletti P.C., Pestka S.;
RT      "Human leukocyte interferon produced by E. coli is biologically
RT      active."
RL      Nature 287:411-416(1980).
CC      [2]
CC      SEQUENCE FROM N.A.
CC      MEDLINE=81148795; PubMed=6163083;
CC      Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
CC      McCandless R., Seeburg P.H., Ullrich A., Yelveton E., Gray P.W.;
CC      "The structure of eight distinct cloned human leukocyte interferon
CC      cDNAs."
CC      Nature 290:20-26(1981).
CC      [3]
CC      SEQUENCE FROM N.A.
CC      MEDLINE=82060261; PubMed=6170983;
CC      Lawn R.M., Gross M., Houck C.M., Franke A.E., Gray P.V.,
CC      Goeddel D.V.;
CC      "DNA sequence of a major human leukocyte interferon gene."
CC      Proc. Natl. Acad. Sci. U.S.A. 78:5435-5439(1981).
CC      [4]
CC      SEQUENCE FROM N.A.
CC      TISSUE=Bone marrow tumor;
CC      MEDLINE=86069501; PubMed=3906813;
CC      Oliver G., Balbas P., Valle F., Soderon X., Bolivar F.;
CC      "Cloning of human leukocyte interferon cDNA and a strategy for its
CC      production in E. coli."
CC      Rev. Latinoam. Microbiol. 27:141-150(1985).
CC      [5]
CC      SEQUENCE OF 7-188 FROM N.A.
CC      MEDLINE=81015442; PubMed=6158094;
CC      Streuli M., Nagata S., Weissmann C.;
CC      "At least three human type alpha interferons: structure of alpha 2."
CC      Science 209:1343-1347(1980).
CC      [6]
CC      SEQUENCE OF 24-188 FROM N.A.
CC      MEDLINE=83299241; PubMed=6310510;
CC      Weber H., Weissmann C.;
CC      "Formation of genes coding for hybrid proteins by recombination
CC      between related, cloned genes in E. coli."
CC      Nucleic Acids Res. 11:5661-5669(1983).
CC      [7]
CC      SEQUENCE OF 24-112 AND 136-188.
CC      MEDLINE=81052321; PubMed=6159537;
CC      Allen G., Fantes K.H.;
CC      "A family of structural genes for human lymphoblastoid
CC      (leukocyte-type) interferon."
CC      Nature 287:408-411(1980).
CC      [8]
CC      DISULFIDE BONDS.
CC      MEDLINE=81123083; PubMed=6162107;
CC      Wetzel R.;
CC      "Assignment of the disulphide bonds of leukocyte interferon."
CC      Nature 289:606-607(1981).
CC      [9]
CC      CARBOHYDRATE-LINKAGE SITE THR-129.
CC      MEDLINE=91264809; PubMed=2049076;
CC      Adolf G.R., Kalsner I., Ahorn H., Maurer Fogy I., Cantelli K.;
CC      "Natural human interferon-alpha 2 is O-glycosylated."
CC      Biochem. J. 276:511-518(1991).
CC      [10]
CC      3D-STRUCTURE MODELING.
CC      MEDLINE=94052087; PubMed=8234245;
CC      Murgolo N.J., Windsor W.T., Hruza A., Reichert P., Tsaropoulos A.,

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OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RT      MEDLINE=81052322; PubMed=6159538;
RA      Goeddel D.V., Yelveton E., Ullrich A., Heyneker H.L., Mizzari G.,
RT      Holmes W., Seeburg P.H., Dull T.J., May L., Stebbins N., Crea R.,
RT      Maeda S., McCandless R., Sloma A., Tabor J.M., Gross M.,
RT      Familletti P.C., Pestka S.;
RT      "Human leukocyte interferon produced by E. coli is biologically
RT      active."
RL      Nature 287:411-416(1980).
CC      [2]
CC      SEQUENCE FROM N.A.
CC      MEDLINE=81148795; PubMed=6163083;
CC      Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
CC      McCandless R., Seeburg P.H., Ullrich A., Yelveton E., Gray P.W.;
CC      "The structure of eight distinct cloned human leukocyte interferon
CC      cDNAs."
CC      Nature 290:20-26(1981).
CC      [3]
CC      SEQUENCE FROM N.A.
CC      MEDLINE=82060261; PubMed=6170983;
CC      Lawn R.M., Gross M., Houck C.M., Franke A.E., Gray P.V.,
CC      Goeddel D.V.;
CC      "DNA sequence of a major human leukocyte interferon gene."
CC      Proc. Natl. Acad. Sci. U.S.A. 78:5435-5439(1981).
CC      [4]
CC      SEQUENCE FROM N.A.
CC      TISSUE=Bone marrow tumor;
CC      MEDLINE=86069501; PubMed=3906813;
CC      Oliver G., Balbas P., Valle F., Soderon X., Bolivar F.;
CC      "Cloning of human leukocyte interferon cDNA and a strategy for its
CC      production in E. coli."
CC      Rev. Latinoam. Microbiol. 27:141-150(1985).
CC      [5]
CC      SEQUENCE OF 7-188 FROM N.A.
CC      MEDLINE=81015442; PubMed=6158094;
CC      Streuli M., Nagata S., Weissmann C.;
CC      "At least three human type alpha interferons: structure of alpha 2."
CC      Science 209:1343-1347(1980).
CC      [6]
CC      SEQUENCE OF 24-188 FROM N.A.
CC      MEDLINE=83299241; PubMed=6310510;
CC      Weber H., Weissmann C.;
CC      "Formation of genes coding for hybrid proteins by recombination
CC      between related, cloned genes in E. coli."
CC      Nucleic Acids Res. 11:5661-5669(1983).
CC      [7]
CC      SEQUENCE OF 24-112 AND 136-188.
CC      MEDLINE=81052321; PubMed=6159537;
CC      Allen G., Fantes K.H.;
CC      "A family of structural genes for human lymphoblastoid
CC      (leukocyte-type) interferon."
CC      Nature 287:408-411(1980).
CC      [8]
CC      DISULFIDE BONDS.
CC      MEDLINE=81123083; PubMed=6162107;
CC      Wetzel R.;
CC      "Assignment of the disulphide bonds of leukocyte interferon."
CC      Nature 289:606-607(1981).
CC      [9]
CC      CARBOHYDRATE-LINKAGE SITE THR-129.
CC      MEDLINE=91264809; PubMed=2049076;
CC      Adolf G.R., Kalsner I., Ahorn H., Maurer Fogy I., Cantelli K.;
CC      "Natural human interferon-alpha 2 is O-glycosylated."
CC      Biochem. J. 276:511-518(1991).
CC      [10]
CC      3D-STRUCTURE MODELING.
CC      MEDLINE=94052087; PubMed=8234245;
CC      Murgolo N.J., Windsor W.T., Hruza A., Reichert P., Tsaropoulos A.,

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RA Baldwin S., Huang E., Pramanik B., Ealick S., Trotta P.P.;  
 RT "A homology model of human interferon alpha-2.";  
 RL Proteins 17:62-74(1993).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE-97148339; PubMed-8994971;  
 RA Radhakrishnan R., Walter L.J., Hruza A., Reichert P., Trotta P.P.,  
 RT Nagabhushan T.L., Walter M.R.;  
 RT "Zinc mediated dimer of human interferon-alpha 2b revealed by X-ray  
 crystallography.";  
 RL Structure 4:1453-1463(1996).  
 RN [12]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE-98118493; PubMed-9417943;  
 RA Klaus W., Gsell B., Labhardt A.M., Wipf B., Senn H.;  
 RT "The three-dimensional high resolution structure of human interferon  
 alpha-2a determined by heteronuclear NMR spectroscopy in solution.";  
 RL J. Mol. Biol. 274:661-675(1997).  
 CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.  
 CC -1- POLYMORPHISM: TWO FORMS, ALPHA-2A AND ALPHA-2B DIFFER BY A SINGLE  
 CC RESIDUE (POSITION 46).  
 CC -1- PHARMACEUTICAL: AVAILABLE UNDER THE NAMES ROBERON-A (ROCHE) OR  
 CC INTERON-A (SCHERING-PLOUGH). USED AS AN ANTICANCER DRUG FOR ITS  
 CC ANTIPROLIFERATIVE ACTIVITY.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
 CC -----  
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 CC EMBL; J00207; AAB59402.1; -  
 CC EMBL; V00544; CAA23805.1; -  
 CC EMBL; V00548; CAA23809.1; -  
 CC EMBL; V00549; CAA23810.1; -  
 CC EMBL; M5486; AAA59181.1; -  
 CC EMBL; M29883; AAA52715.1; -  
 CC EMBL; A04970; CAA00410.1; -  
 CC DR PIR; A01827; IYHUA2.  
 CC DR PIR; A01828; IYHUA3.  
 CC DR PDB; 1RH2; 31-NOV-94.  
 CC DR PDB; 1RH2; 12-NOV-94.  
 CC DR PDB; 1ITF; 03-DEC-97.  
 CC DR GlycoSuiteDB; P01563; -  
 CC MIM; 147562; -  
 CC InterPro: IPR000471; Interferon\_abd.  
 CC Pfam: PF00143; Interferon\_1.  
 CC PRINTS; PR00266; INTERFERONAB.  
 CC DR ProDom; PD000550; Interferon\_abd. 1.  
 CC DR SMART; SM00076; IFabD; 1.  
 CC DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 CC DR Cytokine; Antiviral; Multigene family; Signal; Glycoprotein;  
 CC KW Polymorphism; Pharmaceutical; 3D-structure.  
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 CC FT CARBOHYD 129 129  
 CC FT VARIANT 46 46  
 CC FT O-LINKED (GALNAC. . .).  
 CC FT /FTID-CAR.000049.  
 CC FT K-> R (IN ALPHA-2B).  
 CC FT /FTID-VAR.004012.  
 CC FT SEQUENCE 188 AA; 21550 MW; 101DD21D394CBF97 CRC64;  
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Query Match 85.7%; Score 36; DB 1; Length 188;  
 Best Local Similarity 87.5%; Pred. No. 3.7;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKISP 8  
 ID INAV\_HUMAN STANDARD; PRT; 189 AA.  
 AC P01567;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE INTERFERON ALPHA-7 PRECURSOR (INTERFERON ALPHA-J1) (INTERFERON  
 DE ALPHA-J) (LEIF J).  
 GN IFNA7.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
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 RX MEDLINE-86037205; PubMed-4057246;  
 RA Henko K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,  
 RA Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,  
 RA Todoroko K., Waelchli M., Nagata S., Weissmann C.;  
 RT "Structural relationship of human interferon alpha genes and  
 RT pseudogenes.";  
 RT J. Mol. Biol. 185:227-260(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-83010246; PubMed-6181262;  
 RA Ullrich A., Gray A., Goeddel D.V., Dull J.J.;  
 RT "Nucleotide sequence of a portion of human chromosome 9 containing a  
 RT leukocyte interferon gene cluster.";  
 RT J. Mol. Biol. 156:467-486(1982).  
 CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; V00531; CAA23792.1; -  
 CC EMBL; X02960; CAA26706.1; -  
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 CC DR HSSP; P01563; 2HIE.  
 CC MIM; 147567; -  
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 CC DR ProDom; PD000550; Interferon\_abd. 1.  
 CC DR SMART; SM00076; IFabD; 1.  
 CC DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 CC DR Cytokine; Antiviral; Multigene family; Signal.  
 CC KW Polymorphism; Pharmaceutical; 3D-structure.  
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Query Match 85.7%; Score 36; DB 1; Length 189;  
 Best Local Similarity 87.5%; Pred. No. 3.7;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY      1  LTEKKYSP 8
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Db      154 LMEKKYSP 161

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ID	INAD_HUMAN	STANDARD:	PRT;	189 AA.
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AC	P01570;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	INTERFERON ALPHA-14 PRECURSOR (INTERFERON ALPHA-H) (LEIF H)			
DE	(INTERFERON LAMBDA-2-H).			
GN	IFNA14.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
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NP	SEQUENCE FROM N.A.			
RX	MEDLINE=86037205; PubMed=4057246;			
RA	Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,			
RA	Hochstadt J., Kovacic T., Pasek M., Schaboock A., Schmid J.,			
RA	Todokoro K., Waelchli M., Nagata S., Weissmann C.;			
RT	"Structural relationship of human interferon alpha genes and			
RT	pseudogenes.";			
RL	J. Mol. Biol. 185:227-260(1985).			
RN	[2]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=81201124; PubMed=6165082;			
RA	Lawn R.M., Adelman J., Dull T.J., Gross M., Goeddel D.V., Ullrich A.;			
RT	"DNA sequence of two closely linked human leukocyte interferon			
RT	genes.";			
RL	Science 212:1159-1162(1981).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81148795; PubMed=6163083;			
RA	Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,			
RA	McCandless R., Seeburg P.H., Ullrich A., Yelveton E., Gray P.W.;			
RT	"The structure of eight distinct cloned human leukocyte interferon			
RT	CDNAs.";			
RL	Nature 290:20-26(1981).			
CC	-1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL			
CC	ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:			
CC	A PROTEIN KINASE AND AN OLIGODEHYLATE SYNTHETASE.			
CC	-1- MISCELLANEOUS: A VARIANT SEQUENCE DIFFERS IN 3 POSITIONS, THE LAST			
CC	2 BEING THE RESULT OF A DELETION FOLLOWED BY AN INSERTION.			
CC	-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA			
CC	FAMILY.			
CC	-----			
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
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DR	MM; 147579; -			
DR	InterPro; IPR000471; Interferon_abd.			
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DR	PRINTS; PR00266; INTERFERONAB.			
DR	ProDom; PD000550; Interferon_abd.1.			
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DR	Cytokine; Antiviral; Multigene family; Glycoprotein; signal.			
RT	Signal			

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FT	VARIANT	184	184	/FTID-VAR_004014.
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Query Match	85.7%	Score 36;	DB 1;	Length 189;
Best Local Similarity	87.5%	Pred. NO. 3.7;		
Matches	7:	Conservative	0:	Mismatches
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Db     154 LMEKKYSP 161
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DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	INTERFERON ALPHA PRECURSOR (IFN-ALPHA).			
OS	Felis silvestris catus (Cat).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.			
OX	NCBI_TaxID:9685;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92323151; PubMed=1377975;			
RA	Nakamura N., Sudo T., Matsuda S., Yanai A.;			
RT	"Molecular cloning of feline interferon cDNA by direct expression.";			
RL	Biosci. Biotechnol. Biochem. 56:211-214.(1992).			
RP	[2]			
RX	SEQUENCE OF 1-193 FROM N.A.			
RA	MEDLINE=93291263; PubMed=7685640;			
RT	Ueda Y., Sakurai T., Yanai A.;			
RL	"Homogeneous production of feline interferon in silkworm by replacing single amino acid code in signal peptide region in recombinant baculovirus and characterization of the product.";			
J.	J. Vet. Med. Sci. 55:251-258.(1993).			
CC	-I- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES: A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.			
CC	-I- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.			
CC	-----			
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CC	-----			
DR	EMBL; S62636; AAB27160.2; -			
DR	PIR; JS0664; JS0664.			
DR	HSSP; P01563; ZHE.			
DR	InterPro: IPR000471; Interferon_abd.			
DR	Pfam; PF00143; Interferon_1.			
DR	PRINTS; PR00266; INTERFERONAB.			
DR	ProDom; PD000550; Interferon_abd. 1.			
DR	SMART; SM00076; IFabd. 1.			
DR	PROSITE; PS00252; INTERFERON_A-B_D. 1.			
CC	Cytokine; Antiviral; Signal.			
KT	SIGNAL 1 23 BY SIMILARITY.			

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FT DISULFID 24 123 BY SIMILARITY.
FT DISULFID 52 166 BY SIMILARITY.
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 21 21 S -> V (IN REF. 2).
SQ SEQUENCE 194 AA; 21892 MW; D10E910E3755BFEF CRC64;

Query Match
Best Local Similarity 85.7%; Score 36; DB 1; Length 194;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEEKKYS 8
Db 158 LEEKKYS 165

RESULT 15
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ID IN8_HUMAN
P32881; P09236; P01565;
21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
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GN IFN8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=86037205; Pubmed=4057246;
RA Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,
RA Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,
RA Todokoro K., Melchli M., Nagata S., Weissmann C.;
RT "Structural relationship of human interferon alpha genes and
  pseudogenes.";
RL J. Mol. Biol. 185:227-260(1985).
[2]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=84183614; Pubmed=6325303;
RA Bowden D.W., Mao J., Gill T., Hsiao K., Lillquist J.S., Testa D.,
RA Vovis G.F.;
RT "Cloning of eukaryotic genes in single-strand phage vectors: the
  human interferon genes.";
RL Gene 27:87-99(1984).
[3]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=81174733; Pubmed=6164048;
RA Yelverton E., Leung D., Weck P., Gray P.W., Goeddel D.V.;
RT "Bacterial synthesis of a novel human leukocyte interferon.";
RL Nucleic Acids Res. 9:731-741(1981).
[4]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=81148795; Pubmed=6163083;
RA Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
RA McCandliss R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
RT "The structure of eight distinct cloned human leukocyte interferon
  cDNAs.";
RL Nature 290:20-26(1981).
-1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
  ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
  A PROTEIN KINASE AND AN OLIGODENRYLATE SYNTHETASE.
-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
  FAMILY.
-----
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CC -----
DR EMBL: V00545; CAA23806.1; -
DR EMBL: K01900; AAA52716.1; -
DR EMBL: X03125; CAA26903.1; -
DR EMBL: V00550; CAA23811.1; -
DR PIR: D23753; IVH018.
DR PIR: A01829; IVH044.
DR HSSP: P01563; 2HIE.
DR MIM: 147568; -.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS: PR00266; INTERFERONAB.
DR Prodom: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A.B.D; 1.
KW Cytokine; Antiviral; Multigene family; Signal.
FT SIGNAL 1 23
FT CHAIN 1 23 INTERFERON ALPHA-8.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
FT CONFLICT 8 8 L -> M (IN REF. 3 AND 4).
FT CONFLICT 121 124 SCYW -> VICD (IN REF. 3 AND 4).
SQ SEQUENCE 189 AA; 21989 MW; 83128DA2B0DBB2C1 CRC64;

Query Match
Best Local Similarity 83.3%; Score 35; DB 1; Length 189;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEEKKYS 7
Db 154 LEEKKYS 160

RESULT 16
IN01_HORSE STANDARD; PRT; 195 AA.
ID IN01_HORSE
AC P05001;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-APR-1988 (Rel. 07, Last annotation update)
DE INTERFERON OMEGA-1 PRECURSOR (INTERFERON ALPHA-II-1).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_Taxid=9796;
[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=87053170; Pubmed=3022999;
RA Himmler A., Hauptmann R., Adolf G.R., Swelly P.;
RT "Molecular cloning and expression in Escherichia coli of equine type
  I Interferons.";
RL DNA 5:345-356(1986).
-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
  FAMILY.
-----
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CC -----
DR EMBL: M14544; AAA30955.1; -
DR EMBL: A15991; CAA01259.1; -
DR PIR: E24912; IVH021.
DR HSSP: P01563; 1YTF.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS: PR00266; INTERFERONAB.

```

DR Prodom; PD000550; Interferon\_abd; 1.  
 DR SMART; SM00076; IFabd; 1.  
 DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 KW Cytokine; Glycoprotein; Antiviral; Multigene family; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 195 INTERFERON OMEGA-1.  
 FT DISULFID 24 122 BY SIMILARITY.  
 FT DISULFID 52 162 BY SIMILARITY.  
 FT CARBOHYD 101 101 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 195 AA; 21882 MW; A81C3CF0A7CA9B6E CRC64;

Query Match 83.3%; Score 35; DB 1; Length 195;  
 Best Local Similarity 100.0%; Pred. No. 6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKYS 7  
 Db 154 LTERKYS 160

## RESULT 17

LAD1\_MOUSE STANDARD; PRT; 528 AA.  
 AC P57016;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE LADININ 1 (LAD-1) (LINEAR IGA DISEASE AUTOANTIGEN).  
 GN LAD1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Skin;  
 RA MEDLINE=97224461; PubMed=9119369;  
 RX Mochi K., Megahed M., LaForgia S., Ulto J.;  
 RT "Cloning and chromosomal mapping of mouse ladinin, a novel basement  
 membrane zone component.";  
 RL Genomics 39:323-330(1997).

CC -1- FUNCTION: ANCHORING FILAMENT PROTEIN WHICH IS A COMPONENT OF THE  
 CC BASEMENT MEMBRANE ZONE. MAY CONTRIBUTE TO THE STABILITY OF THE  
 CC ASSOCIATION OF THE EPITHELIAL LAYERS WITH THE UNDERLYING  
 CC MESENCHYME. COULD MAINTAIN DERMAL-EPIDERMAL COHESION.  
 CC -1- SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR MATRIX. LOCALIZED TO  
 CC ANCHORING FILAMENTS UNDERLYING HEMIDESMOSOMES OF THE LAMINA LUCIDA  
 CC OF THE EPIDERMAL BASEMENT MEMBRANE (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN KIDNEY, LUNG AND KERATINOCYTES  
 CC FOLLOWED BY LIVER, SPLEEN AND BRAIN. NOT EXPRESSED IN TESTIS,  
 CC SKELETAL AND HEART MUSCLE AND IN FIBROBLASTS.  
 CC -----  
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 CC -----

DR EMBL; U58011; AAC53044.1; -.  
 DR MGD; MGI:109343; Ladi1.  
 KW Extracellular matrix; Basement membrane; Repeat.  
 FT DOMAIN 28 35  
 FT DOMAIN 184 281 6 X SEK REPEATS.  
 FT REPEAT 184 186 SEK 1.  
 FT REPEAT 190 192 SEK 2.  
 FT REPEAT 202 204 SEK 3.  
 FT REPEAT 208 210 SEK 4.  
 FT REPEAT 269 271 SEK 5.  
 FT REPEAT 279 281 SEK 6.  
 SQ SEQUENCE 528 AA; 58863 MW; 3893C72B0C92609C CRC64;

Query Match 81.0%; Score 34; DB 1; Length 528;  
 Best Local Similarity 75.0%; Pred. No. 25;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKYS 8  
 Db 219 LTERKYS 226

## RESULT 18

INAA\_HUMAN STANDARD; PRT; 189 AA.  
 AC P01566;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE INTERFERON ALPHA-10 PRECURSOR (INTERFERON ALPHA-C) (LEIF C)  
 DE (INTERFERON ALPHA-6L).  
 GN IFNA10.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81148795; PubMed=6163083;  
 RA Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,  
 RA McCandless R., Seeburg P.H., Ullrich A., Vetterton E., Gray P.W.;  
 RT "The structure of eight distinct cloned human leukocyte interferon  
 cDNAs.";  
 RL Nature 290:20-26(1981).

CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
 CC -----

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 CC -----

DR EMBL; V00551; CAA23812.1; -.  
 DR PIR; A01830; IYHVA5.  
 DR HSSP; P01563; IYF.  
 DR MIM; 147577; -.  
 DR InterPro; IPR000471; Interferon\_abd.  
 DR Pfam; PF00143; Interferon; 1.  
 DR PRINTS; PR00266; INTERFERONAB.  
 DR PRODOM; PD000550; Interferon\_abd; 1.  
 DR SMART; SM00076; IFabd; 1.  
 DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 KW Cytokine; Antiviral; Multigene family; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 189 INTERFERON ALPHA-10.  
 FT DISULFID 24 122 BY SIMILARITY.  
 FT DISULFID 52 162 BY SIMILARITY.  
 SQ SEQUENCE 189 AA; 21835 MW; CEC680996FDA706B CRC64;

Query Match 78.6%; Score 33; DB 1; Length 189;  
 Best Local Similarity 75.0%; Pred. No. 14;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTERKYS 8  
 Db 154 LTERKYS 161

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RESULT 19
FVE_FLAVE STANDARD: PRT: 114 AA.
ID FVE_FLAVE
AC P80412;
DR 01-FEB-1995 (Rel. 31, Created)
DR 01-FEB-1995 (Rel. 31, Last sequence update)
DR 01-NOV-1995 (Rel. 32, Last annotation update)
DE IMMUNOMODULATOR PROTEIN FIP-FVE.
OS Flammulina velutipes.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Tricholomataceae; Flammulina.
OX NCBI_TaxID=38945;
RN [1]
RP SEQUENCE.
RX MEDLINE=95220348; PubMed=7705335;
RA Ko J.-L., Hsu C.-I., Lin R.-H., Kao C.-L., Lin J.-Y.;
RT "A new fungal immunomodulatory protein, FIP-five isolated from the
RT edible mushroom, Flammulina velutipes and its complete amino acid
RT sequence."
RT Eur. J. Biochem. 228:244-249(1995).
-1- SIMILARITY: TO IMMUNOGLOBULIN VARIABLE DOMAINS, BUT LACK THE
CONSERVED DISULFIDE BOND.
KW Acetylation.
FT MOD_RES 1 ACETYLATION (BY SIMILARITY).
SQ SEQUENCE 114 AA; 12704 MW; D38C64IDCC112A94 CRC64;

Query Match 76.2%; Score 32; DB 1; Length 114;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 7
Db 42 LTRKYS 48

RESULT 20
INAL_MOUSE STANDARD: PRT: 189 AA.
ID INAL_MOUSE
AC P01572;
DR 21-JUL-1986 (Rel. 01, Created)
DR 21-JUL-1986 (Rel. 01, Last sequence update)
DR 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERFERON ALPHA-1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83168886; PubMed=6188104;
RA Shaw G.D., Boll W., Taira H., Mantel N., Lengyel P., Weissmann C.;
RT "Structure and expression of cloned murine IFN-alpha genes."
RT Nucleic Acids Res. 11:555-573(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85215516; PubMed=2987811;
RA Kelly K.A., Pilth P.M.;
RT "Characterization of a mouse interferon gene locus I. Isolation of a
RT cluster of four alpha interferon genes."
RT Nucleic Acids Res. 13:805-823(1985).
-1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
A PROTEIN KINASE AND AN OLIGONUCLEOTIDE SYNTHETASE.
-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
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DR EMBL; X01974; CA26006.1;
DR PIR; A01836; IWSAL.
DR PIR; A23087; A23087.
DR HSP; P01563; 2HIE.
DR MGD; MGI:107668; Ifnal.
DR InterPro; IP000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; Ifabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
DR Cytokine; Glycoprotein; Antiviral; Multigene family; signal.
KW SIGNAL
FT CHAIN 1 23
FT DISULFID 24 189 INTERFERON ALPHA-1.
FT DISULFID 24 122 BY SIMILARITY.
FT CARBOHYD 52 162 N-LINKED (GLCNAC... ) (PROBABLE).
FT SEQUENCE 101 101
SQ SEQUENCE 189 AA; 21634 MW; 553B4679A4D310BE CRC64;

Query Match 73.8%; Score 31; DB 1; Length 189;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKYS 8
Db 154 LTRKHS 161

RESULT 21
INAL_PIG STANDARD: PRT: 189 AA.
ID INAL_PIG
AC P49879;
DR 01-OCT-1996 (Rel. 34, Created)
DR 01-OCT-1996 (Rel. 34, Last sequence update)
DR 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERFERON ALPHA-1 PRECURSOR (IFN-ALPHA-1).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-DOMESTICA; TISSUE=Liver;
RX MEDLINE=92193689; PubMed=1800582;
RA Lefevre F., la Bonnardiere C., Mege D.;
RT "The porcine family of interferon-omega: cloning, structural
RT analysis, and functional studies of five related genes."
RT J. Interferon Res. 11:341-350(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87035119; PubMed=2945869;
RA Lefevre F., la Bonnardiere C.;
RT "Molecular cloning and sequencing of a gene encoding biologically
RT active porcine alpha-interferon."
RT J. Interferon Res. 6:349-360(1986).
-1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
A PROTEIN KINASE AND AN OLIGONUCLEOTIDE SYNTHETASE.
-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
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CC -----
DR EMBL: X57191; CAA0477.1; -
DR EMBL: M28623; AAA31053.1; -
DR HSSP: P01563; 1TF.
DR InterPro: IPR0004771; Interferon_abd.
DR Pfam: PF00143; Interferon; 1.
DR PRINTS: PR00266; INTERFERONAB.
DR PRODOM: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
DR Cytokine: Antiviral; Multigene family; Signal.
FT CHAIN 1 23
FT SIGNAL 1 23
FT DISULFID 24 189
FT DISULFID 24 122
FT DISULFID 52 162
FT DISULFID 101 101
SQ SEQUENCE 189 AA; 21433 MW; 8C8BEA8DEAAE3334 CRC64;

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Query Match
Best Local Similarity 73.8%; Score 31; DB 1; Length 189;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 LTERKXSP 8
Db 154 LQEKXSP 161

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RESULT 22
IN6_MOUSE
ID IN6_MOUSE STANDARD; PRT; 189 AA.
AC P07350;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERFERON ALPHA-5 PRECURSOR.
GN IFNA5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=85215516; PubMed=2987811;
RA Kelly K.A., Pitba P.M.;
RT "Characterization of a mouse interferon gene locus I. Isolation of a
RT cluster of four alpha interferon genes."
RL Nucleic Acids Res. 13:805-823(1985).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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CC -----
DR EMBL: X01971; CAA26003.1; ALT_SEQ.
DR PIR: C23087; IVMSA5.
DR HSSP: P01563; 2HIE.
DR MGD: MGI:107663; Ifna5.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon; 1.
DR PRINTS: PR00266; INTERFERONAB.
DR PRODOM: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
DR Cytokine: Antiviral; Multigene family; Glycoprotein; Signal.
FT SIGNAL 1 23

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```

FT CHAIN 24 189
FT DISULFID 24 122
FT DISULFID 52 162
FT CARBOHYD 101 101
SQ SEQUENCE 189 AA; 21514 MW; 8BB9CDFD15F5C3BD CRC64;

```

```

Query Match
Best Local Similarity 73.8%; Score 31; DB 1; Length 189;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LTERKXSP 8
Db 154 LQEKXSP 161

```

```

RESULT 23
IN6_MOUSE
ID IN6_MOUSE STANDARD; PRT; 189 AA.
AC P07350;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERFERON ALPHA-6 PRECURSOR.
GN IFNA6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RX STRAIN=BA16/C;
RX MEDLINE=85215516; PubMed=2987811;
RA Kelly K.A., Pitba P.M.;
RT "Characterization of a mouse interferon gene locus I. Isolation of a
RT cluster of four alpha interferon genes."
RL Nucleic Acids Res. 13:805-823(1985).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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CC -----
DR EMBL: X01972; CAA26004.1; -
DR PIR: D23087; IVMSA6.
DR HSSP: P01563; 2HIE.
DR MGD: MGI:107662; Ifna6.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon; 1.
DR PRINTS: PR00266; INTERFERONAB.
DR PRODOM: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
DR Cytokine: Signal; Antiviral; Multigene family; Glycoprotein.
FT SIGNAL 1 23
FT CHAIN 24 189
FT DISULFID 24 122
FT DISULFID 52 162
FT CARBOHYD 101 101
SQ SEQUENCE 189 AA; 21499 MW; A960BC251330664 CRC64;

```

```

Query Match
Best Local Similarity 73.8%; Score 31; DB 1; Length 189;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 LREKRYSP 8  
| | | | |  
DB 154 LREKKHSP 161

## RESULT 24

INAB\_MOUSE STANDARD: PRT: 189 AA.  
AC P17660:  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE INTERFERON ALPHA-8 PRECURSOR.  
GN IFNA8 OR IFA8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89279315; PubMed=2471809;  
RA Navarro S., Dion M., Yodanis G., Berlot-Picard F., Doly J.;  
RT "Isolation and characterization of a functional murine interferon  
alpha gene which is not expressed in fibroblasts upon virus  
induction.";  
RT J. Gen. Virol. 70:1381-1389(1989).  
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.  
CC -1- MISCELLANEOUS: MURINE INTERFERON ALPHA-8 IS NOT EXPRESSED IN  
CC FIBROBLASTS UPON VIRUS INDUCTION.  
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
CC FAMILY.

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CC -----

DR EMBL: D00460; BAA00349.1; -.  
DR HSSP: P01563; 2HIE.  
DR MGD: MGI:107660; Ifna8.  
DR InterPro: IPR000471; Interferon\_abd.  
DR Pfam: PF00143; Interferon\_1.  
DR PRINTS: PR00266; InterferonAB.  
DR ProDom: PD000550; Interferon\_abd; 1.  
DR SMART: SM00076; IFab; 1.  
DR PROSITE: PS00252; INTERFERON\_A-B-D; 1.  
KW Cytokine; Glycoprotein; Antiviral; Multigene family; signal.  
FT CHAIN 1 189 INTERFERON ALPHA-8.  
FT SIGNAL 24 23  
FT DISULFID 24 122 BY SIMILARITY.  
FT DISULFID 52 162 BY SIMILARITY.  
FT CARBOHYD 101 101 N-LINKED (GLCNAC... ) (PROBABLE).  
SQ SEQUENCE 189 AA; 21469 MW; 0960AD342C98EB32 CRC64;

Query Match 73.8%; Score 31; DB 1; Length 189;  
Best Local Similarity 75.0%; Pred. No. 35;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LREKRYSP 8  
| | | | |  
DB 154 LREKKHSP 161

RESULT 25  
INAB\_MOUSE STANDARD: PRT: 190 AA.  
ID INAB\_MOUSE

AC P01573;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE INTERFERON ALPHA-2 PRECURSOR.  
GN IFNA2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83168866; PubMed=6188104;  
RA Shaw G.D., Boll W., Taira H., Mantel N., Lengyel P., Weissmann C.;  
RT "Structure and expression of cloned murine IFN-alpha genes.";  
RT Nucleic Acids Res. 11:555-573(1983).  
RN (2)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85215515; PubMed=2987810;  
RA Zwartthoff E.C., Mooren A.T.A., Trapman J.;  
RT "Organization, structure and expression of murine interferon alpha  
genes.";  
RT Nucleic Acids Res. 13:791-804(1985).

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL: K01238; AAA37887.1; -.  
DR EMBL: X01969; CAA26002.1; -.  
DR PIR: A01837; IVMSA2.  
DR HSSP: P01563; 2HIE.  
DR MGD: MGI:107666; Ifna2.  
DR InterPro: IPR000471; Interferon\_abd.  
DR Pfam: PF00143; Interferon\_1.  
DR PRINTS: PR00266; INTERFERONAB.  
DR ProDom: PD000550; Interferon\_abd; 1.  
DR SMART: SM00076; IFab; 1.  
DR PROSITE: PS00252; INTERFERON\_A-B-D; 1.  
KW Cytokine; Glycoprotein; Antiviral; Multigene family; signal.  
FT CHAIN 1 190 INTERFERON ALPHA-2.  
FT SIGNAL 24 23  
FT DISULFID 24 122 BY SIMILARITY.  
FT DISULFID 52 162 BY SIMILARITY.  
FT CARBOHYD 101 101 N-LINKED (GLCNAC... ) (PROBABLE).  
SQ SEQUENCE 190 AA; 21921 MW; EFA97FC69C300FD5 CRC64;

Query Match 73.8%; Score 31; DB 1; Length 190;  
Best Local Similarity 75.0%; Pred. No. 36;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LREKRYSP 8  
| | | | |  
DB 154 LREKKHSP 161

Search completed: January 15, 2002, 08:44:51  
Job time: 287 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 15, 2002, 08:36:43 ; Search time 22.55 Seconds  
(without alignments)  
27,024 Million cell updates/sec

Title: US-09-424-080a-1

Perfect score: 42  
Sequence: 1 LFEKKYSP 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	72	2 I79343	interferon alpha-T
2	42	100.0	167	2 E25843	interferon alpha-F
3	42	100.0	167	2 D25843	interferon alpha-G
4	42	100.0	176	2 I56314	interferon alpha-H
5	42	100.0	181	2 I56313	interferon alpha-I
6	42	100.0	189	1 IVH016	interferon alpha-2
7	42	100.0	189	1 IVH017	interferon alpha-1
8	42	100.0	189	1 IVH011	interferon alpha-5
9	42	100.0	189	1 IVH01	interferon alpha-1
10	42	100.0	189	1 IVH04B	interferon alpha-1
11	42	100.0	189	1 IVH049	interferon alpha-1
12	42	100.0	189	2 I52347	interferon alpha-M
13	42	100.0	189	2 I84464	interferon alpha-F
14	42	100.0	189	2 I53102	interferon-alpha-J
15	42	100.0	189	2 I51970	interferon precurs
16	36	85.7	165	2 I78570	interferon 2
17	36	85.7	167	2 F25843	interferon alpha-J
18	36	85.7	170	2 A48772	interferon, acyclic
19	36	85.7	184	1 IVH044	interferon alpha-1
20	36	85.7	184	1 IVH042	interferon alpha-1
21	36	85.7	184	1 IVH0A3	interferon alpha-1
22	36	85.7	184	1 IVH0A1	interferon alpha-1
23	36	85.7	188	1 IVH0A2	interferon alpha-2
24	36	85.7	189	1 IVH014	interferon alpha-1
25	36	85.7	189	1 IVH0A0	interferon alpha-7
26	36	85.7	194	2 JS0664	interferon precurs
27	36	85.7	730	2 H86295	hypothetical prote
28	35	83.3	162	2 C25843	interferon alpha-B
29	35	83.3	189	1 IVH044	interferon alpha-4

30	35	83.3	189	1 IVH018	interferon alpha-1
31	35	83.3	195	1 IVH021	interferon alpha-1
32	33	78.6	110	2 F85431	hypothetical prote
33	33	78.6	189	1 IVH0A5	interferon alpha-5
34	33	78.6	221	2 D86051	hypothetical prote
35	32	76.2	114	2 S69147	immunomodulatory p
36	32	76.2	414	2 D96524	protein TIM15.3 f1
37	32	76.2	573	2 T27578	hypothetical prote
38	32	76.2	1528	2 T37308	ATPase homolog - C
39	31	73.8	189	1 IVMSA5	interferon alpha-1
40	31	73.8	189	1 IVMSA1	interferon alpha-1
41	31	73.8	189	1 IVMSA6	interferon alpha-1
42	31	73.8	189	2 S23709	interferon alpha-1
43	31	73.8	189	2 I49773	murine interferon
44	31	73.8	190	1 IVMSA2	interferon alpha-2
45	31	73.8	190	2 JH0468	interferon alpha-1
46	31	73.8	190	2 A24401	interferon alpha-1
47	31	73.8	190	2 I49772	interferon alpha-7
48	31	73.8	190	2 I49775	interferon alpha-B
49	31	73.8	190	2 I49774	interferon -
50	31	73.8	197	2 A70033	carbonic anhydrase

## ALIGNMENTS

RESULT 1  
I79343  
Interferon alpha-T - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 16-Jul-1999  
C:Accession: I79343  
R:lund, B.; Edlund, T.; Lindemaler, W.; Ny, T.; Collins, J.; Lundgren, E.; von Gabai  
Proc. Natl. Acad. Sci. U.S.A. 81, 2435-2439, 1984  
A>Title: Novel cluster of alpha-interferon gene sequences in a placental cosmid DNA 1  
A:Reference number: 158999; MUID:84194022  
A:Accession: I79343  
A:Stetus: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-72 <RES>  
A:Cross-references: GB:K01461; NID:g184575; PIDN:AAA58685.1; PID:g184579  
C:Superfamily: interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 72;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFEKKYSP 8  
DB 65 LFEKKYSP 72

RESULT 2  
E25843  
Interferon alpha-F - human  
N:Alternate names: human leukocyte interferon (IFN)  
C:Species: Homo sapiens (man)  
C:Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 15-Jun-1996  
C:Accession: E25843  
R:Ohara, O.; Teraoka, H.  
FEBS Lett. 211, 78-82, 1987  
A>Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide  
A:Reference number: A91374; MUID:87105954  
A:Accession: E25843  
A:Stetus: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-167 <OH>  
C:Superfamily: interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 0.25;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LTERKYS 8  
|||||||  
Db 132 LTERKYS 139

RESULT 3  
D25843  
Interferon alpha-G - human  
N:Alternate names: human leukocyte interferon (IFN)  
C:Species: Homo sapiens (man)  
C>Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 15-Jun-1996  
C:Accession: D25843  
R:Ohara, O.; Teraoka, H.  
FEBS Lett. 211, 78-82, 1987  
A:Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide gel  
A:Reference number: A91374; MUID:87105954  
A:Accession: D25843  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-167 <OH>  
C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
|||||||  
Db 132 LTERKYS 139

RESULT 4  
I56314  
Interferon-alpha - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
C:Accession: I56314  
R:Lund, B.; von Gabain, A.; Edlund, T.; Ny, T.; Lundgren, E.  
J. Interferon Res. 5, 229-238, 1985  
A:Title: Differential expression of interferon genes in a substrain of Namalva cells.  
A:Reference number: I56314; MUID:85235859  
A:Accession: I56314  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-176 <RES>  
A:Cross-references: GB:M71246; NID:g184572; PIDN:AAA52713.1; PID:g184573  
C:Genetics:  
A:Gene: IFNA  
C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 176;  
Best Local Similarity 100.0%; Pred. No. 0.26;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
|||||||  
Db 141 LTERKYS 148

RESULT 5  
I56313  
Interferon alpha 21 - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
C:Accession: I56313  
R:Gren, E.; Berezin, V.M.; Jansone, I.; Tsimanis, A.; Vishnevsky, Y.; Apsalons, U.  
J. Interferon Res. 4, 609-617, 1984  
A:Title: Novel human leukocyte interferon subtype and structural comparison of alpha int  
A:Reference number: I56313; MUID:85056553

A:Accession: I56313  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-181 <RES>  
A:Cross-references: GB:M28586; NID:g184636; PIDN:AAA36041.1; PID:g306912  
C:Genetics:  
A:Gene: IFNA21  
A:Cross-references: GDB:136360; OMIM:147584  
A:Map position: 9p22-9p22  
C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 181;  
Best Local Similarity 100.0%; Pred. No. 0.27;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
|||||||  
Db 146 LTERKYS 153

RESULT 6  
I1VH016  
Interferon alpha-I-6 precursor - human  
N:Alternate names: HuIFN-alpha-I-6; LeIF K; type I interferon  
C:Species: Homo sapiens (man)  
C>Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 18-Jun-1999  
C:Accession: A23753  
R:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.;  
J. Mol. Biol. 185, 227-260, 1985  
A:Title: Structural relationship of human interferon alpha genes and pseudogenes.  
A:Reference number: A92916; MUID:86037205  
A:Accession: A23753  
A:Molecule type: DNA  
A:Residues: 1-189 <HENC>  
A:Cross-references: GB:X02958; NID:g32662; PIDN:CAA26704.1; PID:g758080  
C:Genetics:  
A:Gene: IFNA6  
A:Cross-references: GDB:136363; OMIM:147566  
A:Map position: 9p22-9p22  
C:Superfamily: Interferon alpha  
C:Keywords: antiviral  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-189/Product: interferon alpha-I-6 #status predicted <MAT>  
F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 100.0%; Score 42; DB 1; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
|||||||  
Db 154 LTERKYS 161

RESULT 7  
I1VH017  
Interferon alpha-5 precursor - human  
N:Alternate names: Interferon alpha-G  
C:Species: Homo sapiens (man)  
C>Date: 01-Sep-1981 #sequence\_revision 29-Jan-1999 #text\_change 21-Jul-2000  
C:Accession: S43716; A01833  
R:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.;  
J. Mol. Biol. 185, 227-260, 1985  
A:Title: Structural relationship of human interferon alpha genes and pseudogenes.  
A:Reference number: A92916; MUID:86037205  
A:Accession: S43716  
A:Molecule type: DNA  
A:Residues: 1-189 <HENC>  
A:Cross-references: EMBL:X02956; NID:g32659; PIDN:CAA26702.1; PID:g758079  
R:Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeb  
Nature 290, 20-26, 1981

A:Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.  
 A:Reference number: A93249; MUID:81148795  
 A:Accession: A01833  
 A:Molecule type: mRNA  
 A:Residues: 57-189 <GOE>  
 A:Cross-references: GB:V00541; GB:J00213; NID:932718; PIDN:CAA23802.1; PID:932719  
 A>Note: eight classes of interferon alpha clones were identified; this sequence is derived from C:Genetics:  
 A:Gene: GDB:IFNA5  
 A:Cross-references: GDB:136362; OMIM:147565  
 A:Map position: 9p22-9p22  
 C:Superfamily: Interferon alpha  
 C:Keywords: antiviral; cytokine; leukocyte  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-189/Product: Interferon alpha-5 #status predicted <MAT>

Query Match 100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LTERKXSP 8  
 |||||||  
 Db 154 LTERKXSP 161

## RESULT 8

IVH041  
 N:Alternate names: Interferon alpha-13; Interferon alpha-D; Interferon alpha-I-1  
 C:Species: Homo sapiens (man)  
 C:Date: 22-May-1981 #sequence\_revision 01-Sep-1981 #text\_change 24-Sep-1999  
 C:Accession: C23285; A91467; A93249; I58213; S43715; S41196; A01826  
 R:Gordon, D.J.; Shepard, H.M.; Goeddel, D.V.  
 M01.Cell: Biol. 5, 768-779, 1985  
 A:Title: Two distinct families of human and bovine interferon-alpha genes are coordinate  
 A:Reference number: A93070; MUID:85187974  
 A:Accession: C23285  
 A:Molecule type: DNA  
 A:Residues: 1-189 <CAP>  
 R:Mantel, N.; Schwarstein, M.; Streuli, M.; Panem, S.; Nagata, S.; Weissmann, C.  
 Gene 10, 1-10, 1980  
 A:Title: The nucleotide sequence of a cloned human leukocyte interferon cDNA.  
 A:Reference number: A91467; MUID:8105094  
 A:Accession: A91467  
 A:Molecule type: mRNA  
 A:Residues: 1-189 <MAN>  
 A:Cross-references: GB:V00537; NID:932711; PIDN:CAA23798.1; PID:932712  
 R:Taniguchi, T.; Mantel, N.; Schwarstein, M.; Nagata, S.; Muramatsu, M.; Weissmann, C.  
 Nature 285, 547-549, 1980  
 A:Title: Human leukocyte and fibroblast interferons are structurally related.  
 A:Reference number: A93226; MUID:80254543  
 A:Accession: A93226  
 A:Molecule type: mRNA  
 A:Residues: 1-189 <MAN>  
 R:Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeburg  
 Nature 290, 20-26, 1981  
 A:Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.  
 A:Reference number: A93249; MUID:81148795  
 A:Accession: A93249  
 A:Molecule type: mRNA  
 A:Residues: 1-136, 'V', 138-189 <GOE>  
 A:Cross-references: GB:V00538; NID:932713; PIDN:CAA23799.1; PID:932714  
 A>Note: eight classes of interferon alpha clones were identified; this sequence is derived from C:Genetics:  
 A:Gene: GDB:IFNA5  
 A:Cross-references: GDB:136362; OMIM:147565  
 A:Map position: 9p22-9p22  
 C:Superfamily: Interferon alpha  
 C:Keywords: antiviral; cytokine; leukocyte  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-189/Product: Interferon alpha-5 #status predicted <MAT>

R:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.;  
 J. Mol. Biol. 185, 227-260, 1985  
 A:Title: Structural relationship of human interferon alpha genes and pseudogenes.  
 A:Reference number: A92916; MUID:86037205  
 A:Accession: S43715  
 A:Molecule type: DNA  
 A:Residues: 1-189 <HEN>  
 A:Cross-references: EMBL:X75934  
 R:Roostoks, N.  
 Submitted to the EMBL Data Library, December 1993  
 A:Reference number: S41196  
 A:Accession: S41196  
 A:Molecule type: DNA  
 A:Residues: 1-9, 'A', 11-189 <ROS>  
 A:Cross-references: EMBL:X75934; NID:9439666; PIDN:CAA53538.1; PID:9439667  
 C:Genetics:  
 A:Gene: GDB:IFNA1  
 A:Cross-references: GDB:136353; OMIM:147660  
 A:Map position: 9p22-9p22  
 C:Superfamily: Interferon alpha  
 C:Keywords: antiviral; cytokine; leukocyte  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-189/Product: Interferon alpha-1 #status predicted <MAT>  
 F:24-122, 52-162/Disulfide bonds: #status predicted

## Query Match

100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LTERKXSP 8  
 |||||||  
 Db 154 LTERKXSP 161

## RESULT 9

IVH041  
 N:Alternate names: Interferon alpha-I-F precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 28-May-1999  
 C:Accession: A01832  
 R:Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeburg  
 Nature 290, 20-26, 1981  
 A:Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.  
 A:Reference number: A93249; MUID:81148795  
 A:Accession: A01832  
 A:Molecule type: mRNA  
 A:Residues: 1-189 <GOE>  
 A:Cross-references: GB:V00540; GB:J00212; NID:932716; PIDN:CAA23801.1; PID:932717  
 A>Note: eight classes of interferon alpha clones were identified; this sequence is derived from C:Genetics:  
 A:Gene: GDB:IFNA1  
 A:Cross-references: GDB:119328; OMIM:147660  
 A:Map position: 9p22-9p22  
 C:Superfamily: Interferon alpha  
 C:Keywords: antiviral  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-189/Product: Interferon alpha-I-F #status predicted <MAT>  
 F:24-122, 52-162/Disulfide bonds: #status predicted

## Query Match

100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LTERKXSP 8  
 |||||||  
 Db 154 LTERKXSP 161

## RESULT 10

IVH04B

interferon alpha-I-4b precursor - human  
 N:Alternate names: HuIFN-alpha-I-4b; type I interferon  
 C:Species: Homo sapiens (man)  
 C>Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 18-Jun-1999  
 C:Accession: E23753  
 R:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov  
 J. Mol. Biol. 185, 227-260, 1985  
 A:Title: Structural relationship of human interferon alpha genes and pseudogenes.  
 A:Reference number: A92916; MUID:86037205  
 A:Accession: E23753  
 A:Molecule type: DNA  
 A:Residues: 1-189 <RES>  
 A:Cross-references: GB:X02955; NID:g32656; PIDN:CAA26701.1; PID:g758078  
 C:Genetics:  
 A:Gene: GDB:IFNA1  
 A:Cross-references: GDB:119328; OMIM:147660  
 A:Map position: 9p22-9p22  
 C:Superfamily: Interferon alpha  
 C:Keywords: antiviral  
 A:Title: Domain: signal sequence #status predicted <SIG>  
 F:24-189/Product: interferon alpha-I-4b #status predicted <MAT>  
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTRKXSP 8  
 Db 154 LTRKXSP 161

RESULT 11  
 IYHUA9  
 Interferon alpha-17 precursor - human  
 N:Alternate names: Interferon alpha-9; Interferon alpha-I'  
 C:Species: Homo sapiens (man)  
 C>Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 21-Jul-2000  
 C:Accession: A01835; A22255; C42753  
 R:Law, R.M.; Adelstein, J.; Dull, T.J.; Gross, M.; Goeddel, D.; Ullrich, A.  
 Science 212, 1159-1162, 1981  
 A:Title: DNA sequence of two closely linked human leukocyte interferon genes.  
 A:Reference number: A94255; MUID:81201124  
 A:Accession: A01835  
 A:Molecule type: DNA  
 A:Residues: 1-189 <LAM>  
 A:Cross-references: GB:J00216; GB:V00332; NID:g32633; PIDN:CAA23793.1; PID:g32634  
 R:Mizoguchi, J.; Pitsha, P.M.; Raj, N.B.K.  
 DNA 4, 221-232, 1985  
 A:Title: Efficient expression in Escherichia coli of two species of human interferon-alf  
 A:Reference number: A22255; MUID:85229953  
 A:Accession: A22255  
 A:Molecule type: mRNA  
 A:Residues: 1-56, 'H', 58-189 <MT2>  
 A:Cross-references: GB:M1026; NID:g184612; PIDN:AAA52725.1; PID:g306908  
 R:Zoon, K.C.; Miller, D.; Bekisz, J.; zur Nedden, D.; Enterline, J.C.; Nguyen, N.Y.; Hu,  
 J. Biol. Chem. 267, 15210-15216, 1992  
 A:Title: Purification and characterization of multiple components of human lymphoblastoid  
 A:Reference number: A42753; MUID:92340576  
 A:Accession: C42753  
 A:Molecule type: protein  
 A:Residues: 'X', 25-50, 'XX', 53-56 <ZOO>  
 C:Genetics:  
 A:Gene: GDB:IFNA17  
 A:Cross-references: GDB:136358; OMIM:147583  
 A:Map position: 9p22-9p22  
 C:Superfamily: Interferon alpha  
 C:Keywords: leukocyte  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-189/Product: interferon alpha-17 #status predicted <MAT>  
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTRKXSP 8  
 Db 154 LTRKXSP 161

RESULT 12  
 I52347  
 Interferon alpha-M1 precursor - human  
 C:Species: Homo sapiens (man)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
 C:Accession: I52347  
 R:Linane, A.W.; Bellharz, M.W.; McMullen, G.L.; Macreadie, I.G.; Murphy, M.; Nisbet,  
 Biochem. Int. 8, 725-732, 1984  
 A:Title: Nucleotide sequence and expression in E. coli of a human interferon-alpha ge  
 A:Reference number: I52347; MUID:84307815  
 A:Accession: I52347  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-189 <RES>  
 A:Cross-references: GB:M27318; NID:g184617; PIDN:AAA52726.1; PID:g306909  
 C:Genetics:  
 A:Gene: IFNA  
 C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTRKXSP 8  
 Db 154 LTRKXSP 161

RESULT 13  
 I84464  
 Interferon-alpha-F - human  
 C:Species: Homo sapiens (man)  
 C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 16-Jul-1999  
 C:Accession: I84464; I37583  
 R:Gren, E.Y.; Betzlin, V.M.; Tsimanis, A.Y.; Apsalon, U.R.; Vishnevskii, Y.I.; Yansone  
 A.; Lozna, V.P.; Kavan, V.M.; Efimov, V.A.; Sverdlov, E.D.  
 Dokl. Biochem. 269, 91-95, 1983  
 A:Title: A new type of leukocytic interferon.  
 A:Reference number: I37583  
 A:Accession: I84464  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-189 <RES>  
 A:Cross-references: GB:M12350; NID:g184598; PIDN:AAA52718.1; PID:g306906  
 A:Accession: I37583  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-189 <RES>  
 A:Cross-references: EMBL:X00145; NID:g32724; PIDN:CAA24980.1; PID:g32725  
 C:Genetics:  
 A:Gene: IFNA  
 C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTRKXSP 8  
 Db 154 LTRKXSP 161

## RESULT 14

I53102

Interferon-alpha-J1 - human

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999

C:Accession: I53102

R:Cohen, S.; Velian, B.; Grosfeld, H.; Shalita, Z.; Leitner, M.; Shaffer, A.

Dev. Biol. Stand. 60, 111-122, 1985

A:Title: Cloning, expression and biological activity of a new variant of human interferon

A:Reference number: I53102; MUID:86005847

A:Accession: I53102

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-189 &lt;RES&gt;

A:Cross-references: GB:M34913; NID:g184614; PIDN:AAA36039.1; PID:g184615

C:Superfamily: Interferon alpha

## Query Match

Best Local Similarity 100.0%; Score 42; DB 2; Length 189;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRKXSP 8

I|||||I

DB 154 LTRKXSP 161

## RESULT 15

I51970

Interferon precursor - human

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999

C:Accession: I51970

R:Gavelier, V.I.; Zlochevsky, M.L.; Sorokin, A.V.; Natoditskaya, V.A.; Bolotin, A.P.; De

Antibiot. Med. Biotechnol. 31, 352-356, 1986

A:Title: Cloning and the determination of the nucleotide sequences in 2 genes of human

A:Reference number: I51970; MUID:87024453

A:Accession: I51970

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-189 &lt;RES&gt;

A:Cross-references: GB:M38289; NID:g186407; PIDN:AAA59165.1; PID:g186408

C:Genetics:

A:Gene: IFNA

C:Superfamily: Interferon alpha

## Query Match

Best Local Similarity 100.0%; Score 42; DB 2; Length 189;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRKXSP 8

I|||||I

DB 154 LTRKXSP 161

## RESULT 16

I78570

alpha 2 Interferon - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 16-Jul-1999

C:Accession: I78570

R:Weber, H.; Weismann, C.

Nucleic Acids Res. 11, 5661-5669, 1983

A:Title: Formation of genes coding for hybrid proteins by recombination between related

A:Reference number: I58213; MUID:8329241

A:Accession: I78570

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-165 &lt;RES&gt;

A:Cross-references: GB:M29883; NID:g184585; PIDN:AAA52715.1; PID:g386795

C:Genetics:

A:Gene: IFNA  
C:Superfamily: Interferon alpha

## Query Match

Best Local Similarity 85.7%; Score 36; DB 2; Length 165;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTRKXSP 8

I|||||I

DB 130 LTRKXSP 137

## RESULT 17

F25843

Interferon alpha-J - human

N:Alternate names: human leukocyte interferon (IFN)

C:Species: Homo sapiens (man)

C:Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 15-Jun-1996

C:Accession: F25843

R:Ohara, O.; Terakura, H.

FEBS Lett. 211, 78-82, 1987

A:Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide

A:Reference number: A91374; MUID:87105954

A:Accession: F25843

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-167 &lt;OHA&gt;

C:Superfamily: Interferon alpha

## Query Match

Best Local Similarity 85.7%; Score 36; DB 2; Length 167;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTRKXSP 8

I|||||I

DB 132 LTRKXSP 139

## RESULT 18

A48772

Interferon, atypical type I precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 24-Nov-1999

C:Accession: A48772

R:DeFeve, F.; Boulay, V.

J. Biol. Chem. 268, 19760-19768, 1993

A:Title: A novel and atypical type one interferon gene expressed by trophoblast durin

A:Reference number: A48772; MUID:93374975

A:Accession: A48772

A:Status: preliminary

A:Molecule type: DNA; mRNA

A:Residues: 1-170 &lt;LEF&gt;

A:Cross-references: GB:22706; NID:g414202; PIDN:CAA80407.1; PID:g414203

C:Genetics:

A:Introns: #status absent

C:Superfamily: Interferon alpha

## Query Match

Best Local Similarity 85.7%; Score 36; DB 2; Length 170;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTRKXSP 8

I|||||I

DB 146 LTRKXSP 153

## RESULT 19

IVH04

Interferon alpha-I-4 precursor - horse

N:Alternate names: EdIFN-alpha-I-4; type I interferon

C:Species: Equus caballus (domestic horse)  
 C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 18-Jun-1999  
 C:Accession: D24912  
 R:Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.  
 DNA 5, 345-356, 1986  
 A:Title: Molecular cloning and expression in Escherichia coli of equine type I interferon  
 A:Reference number: A90956; MUID:87053170  
 A:Accession: D24912  
 A:Molecule type: DNA  
 A:Residues: 1-184 <HIM>  
 A:Cross-references: GB:M4543; NID:9164224; PIDN:AAA30952.1; PID:9164225  
 C:Superfamily: interferon alpha  
 C:Keywords: antiviral  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-184/Product: interferon alpha-I-4 #status predicted <MAT>  
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 85.7%; Score 36; DB 1; Length 184;  
 Best Local Similarity 87.5%; Pred. No. 4.8;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
 I | | | | |  
 Db 154 LOEKXKXSP 161

## RESULT 20

IVHOA2  
 Interferon alpha-I-2 precursor - horse  
 N:Alternate names: EqIFN-alpha-I-2; type I interferon  
 C:Species: Equus caballus (domestic horse)  
 C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 18-Jun-1999  
 C:Accession: B24912  
 R:Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.  
 DNA 5, 345-356, 1986  
 A:Title: Molecular cloning and expression in Escherichia coli of equine type I interferon  
 A:Reference number: A90956; MUID:87053170  
 A:Accession: B24912  
 A:Molecule type: DNA  
 A:Residues: 1-184 <HIM>  
 A:Cross-references: GB:M4541; NID:9164218; PIDN:AAA30950.1; PID:9164221  
 C:Superfamily: interferon alpha  
 C:Keywords: antiviral  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-184/Product: interferon alpha-I-2 #status predicted <MAT>  
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 85.7%; Score 36; DB 1; Length 184;  
 Best Local Similarity 87.5%; Pred. No. 4.8;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
 I | | | | |  
 Db 154 LOEKXKXSP 161

## RESULT 21

IVHOA3  
 Interferon alpha-I-3 precursor - horse  
 N:Alternate names: EqIFN-alpha-I-3; type I interferon  
 C:Species: Equus caballus (domestic horse)  
 C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 18-Jun-1999  
 C:Accession: C24912  
 R:Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.  
 DNA 5, 345-356, 1986  
 A:Title: Molecular cloning and expression in Escherichia coli of equine type I interferon  
 A:Reference number: A90956; MUID:87053170  
 A:Accession: C24912  
 A:Molecule type: DNA  
 A:Residues: 1-184 <HIM>  
 A:Cross-references: GB:M4542; NID:9164222; PIDN:AAA30951.1; PID:9164223

C:Superfamily: interferon alpha  
 C:Keywords: antiviral  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-184/Product: interferon alpha-I-3 #status predicted <MAT>  
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 85.7%; Score 36; DB 1; Length 184;  
 Best Local Similarity 87.5%; Pred. No. 4.8;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
 I | | | | |  
 Db 154 LOEKXKXSP 161

## RESULT 22

IVHOA1  
 Interferon alpha-I-1 precursor - horse  
 N:Alternate names: EqIFN-alpha-I-1; type I interferon  
 C:Species: Equus caballus (domestic horse)  
 C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 18-Jun-1999  
 C:Accession: A24912  
 R:Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.  
 DNA 5, 345-356, 1986  
 A:Title: Molecular cloning and expression in Escherichia coli of equine type I interferon  
 A:Reference number: A90956; MUID:87053170  
 A:Accession: A24912  
 A:Molecule type: DNA  
 A:Residues: 1-184 <HIM>  
 A:Cross-references: GB:M4540; NID:9164226; PIDN:AAA30953.1; PID:9164227  
 C:Superfamily: interferon alpha  
 C:Keywords: antiviral  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-184/Product: interferon alpha-I-1 #status predicted <MAT>  
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 85.7%; Score 36; DB 1; Length 184;  
 Best Local Similarity 87.5%; Pred. No. 4.8;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKXSP 8  
 I | | | | |  
 Db 154 LOEKXKXSP 161

## RESULT 23

IVHOA2  
 Interferon alpha-2 precursor (allele a) [validated] - human  
 N:Alternate names: IFN-alpha2; interferon alpha-2; leukocyte interferon  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Oct-1980 #sequence\_revision 01-Sep-1991 #text\_change 08-Dec-2000  
 C:Accession: A93234; D93249; A93888; A94252; A01828; C61478; S15848;  
 R:Goeddel, D.V.; Yelverton, E.; Ullrich, A.; Heyneker, H.L.; Moczart, G.; Holmes, W.  
 ss, M.; Familletti, P.C.; Pestka, S.  
 Nature 287, 411-416, 1980  
 A:Title: Human leukocyte interferon produced by Escherichia coli is biologically active  
 A:Reference number: A93234; MUID:81052322  
 A:Accession: A93234  
 A:Molecule type: DNA  
 A:Residues: 1-188 <GOB>  
 A:Cross-references: GB:V00544; NID:932730; PIDN:CAA23805.1; PID:932731  
 A:Experimental source: Clone pL31  
 R:Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandlish, R.; Seeb  
 Nature 290, 20-26, 1981  
 A:Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.  
 A:Reference number: A93249; MUID:81148795  
 A:Accession: D93249  
 A:Molecule type: mRNA  
 A:Residues: 1-188 <GO2>  
 A:Cross-references: GB:V00549; NID:932744; PIDN:CAA23810.1; PID:932745  
 A:Note: eight classes of interferon alpha clones were identified; this sequence is de

R:Lawn, R.M.; Gross, M.; Houck, C.M.; Franke, A.E.; Gray, P.V.; Goeddel, D.V.  
 Proc. Natl. Acad. Sci. U.S.A. 78, 5435-5439, 1981  
 A:Title: DNA sequence of a major human leukocyte interferon gene.  
 A:Reference number: A93888; MUID:82060261  
 A:Accession: A93888  
 A:Molecule type: DNA  
 A:Residues: 1-45, 'R', 47-188 <LAN>  
 A:Cross-references: GB:J00207; NID:q184581; PIDN:AA59402.1; PID:q386793  
 A:Experimental source: clone lambda-alpha-2  
 R:Olliver, G.; Balbas, P.; Valle, F.; Soberon, X.; Bolivar, F.  
 Rev. Latinoam. Microbiol. 27, 141-150, 1985  
 A:Title: Cloning of human leukocyte interferon cDNA and a strategy for its production  
 A:Reference number: I59458; MUID:86069501  
 A:Accession: I59458  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-188 <RES>  
 A:Cross-references: GB:M54886; NID:q186498; PIDN:AA59181.1; PID:q186499  
 R:Streuli, M.; Nagata, S.; Weissmann, C.  
 Science 209, 1343-1347, 1980  
 A:Title: At least three human type alpha interferons: structure of alpha2.  
 A:Reference number: A94252; MUID:81015442  
 A:Accession: A94252  
 A:Molecule type: mRNA  
 A:Residues: 7-45, 'R', 47-188 <STR>  
 A:Cross-references: GB:V00348; NID:q32740; PIDN:CAA33809.1; PID:q32741  
 R:Ohara, O.; Teraoka, H.  
 FEBS Lett. 211, 78-82, 1987  
 A:Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide gel  
 A:Reference number: A91374; MUID:87105954  
 A:Accession: A25843  
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 'M', 24-188 <CHA>  
 A:Note: engineered sequence of mature form expressed in *Escherichia coli*  
 R:Allen, G.; Fantes, K.H.  
 Nature 287, 408-411, 1980  
 A:Title: A family of structural genes for human lymphoblastoid (leukocyte-type) interferon  
 A:Reference number: A01828; MUID:81052321  
 A:Accession: A01828  
 A:Molecule type: protein  
 A:Residues: 24-42, 'Z', 44-45, 'R', 47-74, 'A', 76, 'S', 78-98, 'X', 100-105, 'D', 107-109, 'P', 111-113  
 A:Note: residues at positions 83, 86, and 139 may be Ile or possibly Leu; those at position 57-Arg, 75-Thr, 77-Pro, and 96-Glx were also found  
 R:Fukuda, S.; Ando, S.; Sanou, O.; Tanaka, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; Arimura, H.  
 Lymphokine Res. 7, 175-185, 1988  
 A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and interferon-gamma  
 A:Reference number: A61478; MUID:88301617  
 A:Accession: C61478  
 A:Molecule type: protein  
 A:Residues: 24-45, 'R', 47-53 <FKK>  
 A:Experimental source: B-cell lymphoblastoid cell line BALL-1  
 R:Adolf, G.R.; Kalsner, I.; Ahorn, H.; Maurer-Fogy, I.; Cantell, K.  
 Biochem. J. 276, 511-518, 1991  
 A:Title: Natural human interferon-alpha-2 is O-glycosylated.  
 A:Reference number: S15848; MUID:91264809  
 A:Accession: S15848  
 A:Molecule type: protein  
 A:Residues: 24-45, 'R', 47-53 <BIO>  
 A:Experimental source: leukocytes  
 R:Zoon, K.C.; Miller, D.; Bekisz, J.; zur Nedden, D.; Enterline, J.C.; Nguyen, N.Y.; Hu, J.; Biol. Chem. 267, 15210-15216, 1992  
 A:Title: Purification and characterization of multiple components of human lymphoblastoid interferon  
 A:Reference number: A42753; MUID:92340576  
 A:Accession: B42753  
 A:Molecule type: protein  
 A:Residues: 'X', 25-45, 'R', 47-51, 'X', 53-55, 'XX', 58-65 <ZOO>  
 A:Experimental source: Sendai virus-induced Namalwa cells  
 R:Metzel, R.  
 Nature 289, 606-607, 1981  
 A:Title: Assignment of the disulphide bonds of leukocyte interferon.  
 A:Reference number: A93244; MUID:81123083  
 A:Accession: A93244  
 A:Contents: annotation; disulfide bonds

R:Murgolo, N.J.; Windsor, W.T.; Hruza, A.; Reichert, P.; Tsaropoulos, A.; Baldwin, S.  
 Proteins 17, 62-74, 1993  
 A:Title: A homology model of human interferon alpha-2.  
 A:Reference number: A44748; MUID:94052087  
 A:Contents: annotation; theoretical model  
 R:Gewert, D.; Salom, C.; Barber, K.; Macbride, S.; Cooper, H.; Lewis, A.; Wood, J.; C.  
 J. Interferon Res. 13, 227-231, 1993  
 A:Title: Analysis of interferon-alpha 2 sequences in human genomic DNA.  
 A:Reference number: I56312; MUID:93375201  
 A:Accession: I56312  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-72 <REW>  
 A:Cross-references: GB:S64979; NID:q408874; PIDN:AA013960.1; PID:q4261660  
 R:Zhao, X.X.; Li, B.L.; Jang, J.A.; Van Riper, G.; Pestka, S.  
 Anal. Biochem. 178, 342-347, 1989  
 A:Title: Construction and phosphorylation of a fusion protein Hu-IFN-alpha A/gamma.  
 A:Reference number: I36908; MUID:89321045  
 A:Accession: I36909  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 'M', 24-188 <RE2>  
 A:Cross-references: EMBL:X15631; NID:q22771; PIDN:CAA33638.1; PID:q22772  
 C:Genetics:  
 A:Gene: GDB:IFNA2  
 A:Cross-references: GDB:136359; OMIM:147562  
 A:Map position: 9p22-9p22  
 C:Superfamily: interferon alpha  
 C:Keywords: antiviral; cytokine; glycoprotein; leukocyte  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-188/Product: interferon alpha-2 #status experimental <MAT>  
 F:24-121,52-161/Disulfide bonds: #status experimental  
 F:129/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 85.7% Score 36; DB 1; Length 188;  
 Best Local Similarity 87.5% Pred. No. 4.9;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 LFEKRYSP 8  
 DB 153 LFEKRYSP 160

RESULT 24  
 IYHUI4  
 Interferon alpha-I-14 precursor [validated] - human  
 M:Alternate names: HuIFN-alpha-I-14; lambda-2-h; type I interferon  
 C:Species: Homo sapiens (man)  
 C:Date: 01-Sep-1981 #sequence revision 01-Sep-1981 #text change 08-Dec-2000  
 C:Accession: A92916; A94255; B93249; PC2203; A01834; C23753  
 R:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.;  
 J. Mol. Biol. 185, 227-260, 1985  
 A:Title: Structural relationship of human interferon alpha genes and pseudogenes.  
 A:Reference number: A92916; MUID:86037205  
 A:Accession: A92916  
 A:Molecule type: DNA  
 A:Residues: 1-189 <HEN>  
 A:Cross-references: GB:X02959; NID:q32650; PIDN:CAA26705.1; PID:q758076  
 R:Lawn, R.M.; Adelstein, J.; Dull, T.J.; Gross, M.; Goeddel, D.; Ullrich, A.  
 Science 212, 1159-1162, 1981  
 A:Title: DNA sequence of two closely linked human leukocyte interferon genes.  
 A:Reference number: A94255; MUID:81201124  
 A:Accession: A94255  
 A:Molecule type: DNA  
 A:Residues: 1-189 <LAN>  
 A:Cross-references: GB:V00533; GB:J00215; NID:q32635; PIDN:CAA23794.1; PID:q32636  
 R:Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeb  
 Nature 290, 20-26, 1981  
 A:Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.  
 A:Reference number: A93249; MUID:81148795  
 A:Accession: B93249  
 A:Molecule type: mRNA

A:Residues: 1-174, 'F', 176-189 <GOE>  
 A:Cross-references: GB:V00542; GB:J00214; NID:932720; PIDN:CAA23803.1; PID:932721  
 A:Note: a variant sequence differs from that shown in having 175-Phe, 182-Lys, and 184-G  
 R:Shiono, H.; Koga, J.; Uemura, H.; Matsuo, A.  
 Biosci. Biotechnol. Biochem. 58, 1714-1715, 1994  
 A:Title: Identification of glycosylated subtypes of interferon-alpha produced by human 1  
 A:Reference number: PC2203; MUID:95036878  
 A:Accession: PC2203  
 A:Molecule type: protein  
 A:Residues: 'X', 25-43 <SHI>  
 A:Experimental source: leukocyte  
 C:Genetics:  
 A:Gene: GDB:IFNA14  
 A:Cross-references: GDB:136356; OMIM:147579  
 A:Map position: 9p22-9p22  
 C:Superfamily: interferon alpha  
 C:Keywords: antiviral; glycoprotein  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-189/Product: interferon alpha-I-14 #status experimental <MAT>  
 F:24-122,52-162/Disulfide bonds: #status predicted  
 F:25,95/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 85.7%; Score 36; DB 1; Length 189;  
 Best Local Similarity 87.5%; Pred. No. 4.9;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LTERKYP 8  
 Db 154 LMEKKYP 161

## RESULT 25

IVH0A0  
 Interferon alpha-7 precursor - human  
 N:Alternate names: Interferon alpha-J; LeIF J  
 C:Species: Homo sapiens (man)  
 C>Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 18-Jun-1999  
 C:Accession: A01831; S43717  
 R:Ullrich, A.; Gray, A.; Goeddel, D.V.; Dull, T.J.  
 J. Mol. Biol. 156, 467-486, 1982  
 A:Title: Nucleotide sequence of a portion of human chromosome 9 containing a leukocyte 1  
 A:Reference number: A01831; MUID:83010248  
 A:Accession: A01831  
 A:Molecule type: DNA  
 A:Residues: 1-189 <UUL>  
 A:Cross-references: GB:V00531; NID:932631; PIDN:CAA23792.1; PID:932632; DDBJ:J00217  
 A:Note: this interferon is derived from a gene referred to as J by the authors  
 R:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov  
 J. Mol. Biol. 185, 227-260, 1985  
 A:Title: Structural relationship of human interferon alpha genes and pseudogenes.  
 A:Reference number: A92916; MUID:86037205  
 A:Accession: S43717  
 A:Molecule type: DNA  
 A:Residues: 1-189 <HEN>  
 A:Cross-references: EMBL:X02960; NID:932665; PIDN:CAA26706.1; PID:9758081  
 C:Genetics:  
 A:Gene: GDB:IFNA7  
 A:Cross-references: GDB:136364; OMIM:147567  
 A:Map position: 9p22-9p22  
 C:Superfamily: interferon alpha  
 C:Keywords: antiviral; cytokine; leukocyte  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-189/Product: interferon alpha-7 #status predicted <MAT>  
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 85.7%; Score 36; DB 1; Length 189;  
 Best Local Similarity 87.5%; Pred. No. 4.9;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKYP 8  
 Db 154 LMEKKYP 161

Db 154 LMEKKYP 161

Search completed: January 15, 2002, 08:40:57  
 Job time: 254 sec